

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 30, 2004, 14:49:24 ; Search time 5672.5 seconds

(without alignments)
10716.922 Million cell updates/sec

Title: US-09-737-297-1

Sequence: 1486
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Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 2888711 seqs, 2045491386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

GenEmbl:*

1: gb_ba:*

2: gb_hlg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pac:*

7: gb_ph:*

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9: gb_pr:*

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14: gb_vl:*

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18: em_in:*

19: em_mu:*

20: em_om:*

21: em_or:*

22: em_ov:*

23: em_ph:*

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25: em_pl:*

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32: em_hlg_other:*

33: em_hlg_mus:*

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41: em_higo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1486	100.0	1486	1	MPR238597
2	1486	100.0	1486	6	AX175613
3	1400.8	94.3	1421	1	AF468256
4	1396.6	94.0	1425	1	AF468385
5	1372	92.3	1372	1	AY092066
6	1370	92.2	1449	1	AB074194
7	1344	90.4	1419	1	AB074193
8	1289.4	86.8	1448	1	AF173967
9	1272	85.6	1455	1	AY028204
10	1265.6	85.2	1534	1	AF063027
11	1265.2	85.1	1475	1	AY028196
12	1251.8	84.2	1481	6	AX175616
13	1197.8	80.6	1343	1	AF321017
14	1190.2	80.1	1467	1	WV16SRNA
15	1177.6	79.2	1417	1	AF468267
16	1177	79.2	1412	1	AF468285
17	1174.2	79.0	1501	1	AF382102
18	1171	78.8	1537	1	AB086227
19	1165.2	78.4	1495	1	AF505730
20	1159.8	78.0	1531	1	PTF492826
21	1159.8	78.0	1538	1	AB001441
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23	1159.8	78.0	1538	1	AB001446
24	1159.8	78.0	1538	1	AB001447
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ALIGNMENTS

RESULT 1

MPR238597

LOCUS MPR238597 1486 bp

DEFINITION Marinomonas protea 16S rRNA gene.

ACCESSION AJ238597.1 GI:4741661

VERSION 16S ribosomal RNA; 16S rRNA gene.

KEYWORDS

SOURCE Marinomonas protea

ORGANISM Marinomonas protea

REFERENCE 1

AUTHORS Mills, S.V., Stewart, G.S.A.B., Laybourn-Parry, J. and Hill, P.J.

TITLE Marinomonas protea sp. nov., a novel Antarctic bacterium isolated from Ace Lake, Eastern Antarctica

Marinomonas.

Marinomonas protea

Bacteria; Proteobacteria; Gammaproteobacteria; Oceanospirillales;

linear BCT 03-MAY-1999

JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1486)
AUTHORS Mills S.V.
TITLE Direct Submission
JOURNAL Submitted (28-Apr-1999) Mills S.V., Food Microbiology, University
of Nottingham, Sutton Bonington Campus, Leicestershire, LE12 5RD,
UNITED KINGDOM

FEATURES

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/db_xref="taxon:32949"
/country="Antarctica:Vestfold Hills, Ace Lake"

gene

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rRNA

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Matches 1486; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1201 GGGCTACACACGTGCTCAATGCGTATACAGAGGCTTGCAAGCTAGCATAGTACGCA 1260
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RESULT 2
AX175613 1486 bp DNA linear PART 03-JUL-2001
LOCUS Sequence 1 from Patent WO0144275.
DEFINITION AX175613
ACCESSION AX175613
VERSION AX175613.1 GI:14598933
KEYWORDS
SOURCE
ORGANISM
Marinomonas protea
Bacteria; Proteobacteria; Gammaproteobacteria; Oceanospirillales;
Marinomonas.
REFERENCE
1
AUTHORS Berry M.J., Griffiths A.U., Hill P.J., Laybourne-Parry J. and
Mills S.V.
TITLE Processes and organisms for the production of anti-freeze proteins
JOURNAL Patent: WO 0144275-A 1 21-JUN-2001;
FEATURES
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/organism="Marinomonas protea"
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ORIGIN           /db_xref="taxon:922949"
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QY	61	GGAGCTTGTCTGTGACGAGCGCGAGCGGTAAGTAAACGCGTAGAATCTGCTAGT	120
Db	61	GGAGCTTGTCTGTGACGAGCGCGAGCGGTAAGTAAACGCGTAGAATCTGCTAGT	120
QY	121	AGAGGGGGGCAACATGTGGAAACGATGTCTAATCCGCATACGCCCTGAGGGGGAAAG	180
Db	121	AGAGGGGGGCAACATGTGGAAACGATGTCTAATCCGCATACGCCCTGAGGGGGAAAG	180
QY	181	GGGGACTCTTGGAGACCTTCGCGATTATGATGAGACCTGCGTAGATTAGCTAGTGGTAG	240
Db	181	GGGGACTCTTGGAGACCTTCGCGATTATGATGAGACCTGCGTAGATTAGCTAGTGGTAG	240
QY	241	GGTAAAGSCTTACCAAGGCGACGATCTCTAACTGTGTGAGAGATGACCACTGCACTG	300
Db	241	GGTAAAGSCTTACCAAGGCGACGATCTCTAACTGTGTGAGAGATGACCACTGCACTG	300
QY	301	GGACGTGAGCAAGGCGCCAGACTCTTACCGGAGGAGACGATGTGGGAATATTGACAAATGGG	360
Db	301	GGACGTGAGCAAGGCGCCAGACTCTTACCGGAGGAGACGATGTGGGAATATTGACAAATGGG	360
QY	361	CGCAAGCTCGATCCAGCATGCGCGGTGTGTGAAGAAGGCTTAGGATTGTAAAGCACTT	420
Db	361	CGCAAGCTCGATCCAGCATGCGCGGTGTGTGAAGAAGGCTTAGGATTGTAAAGCACTT	420
QY	421	TCAGGGGTGAGAAAGGTGTATAGTAACTGATATCATCTTGAACGTTAGCCCGAAGA	480
Db	421	TCAGGGGTGAGAAAGGTGTATAGTAACTGATATCATCTTGAACGTTAGCCCGAAGA	480
QY	481	AGACACGGGTAACTGTGTGACAGACGCGCGGTAAATCAAGGGTCCAAAGCTTAATCGG	540
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QY	541	AATTACTGSGCTAAAGCGCGGTAGGTGTTTGTTAATCGGATGTCAATTCGCAAGGC	600
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QY	601	TCACCTTGGAAATGSCACCCGATCTGCTAGCTAGATGTGTAGAGGGGTGTGGATT	660
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QY	841	GCTTAACGCATTAAGTAGACCGCTGTGGGAGTAGACGCGCAAGTTAAATCTGAATAGAT	900
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QY	901	TGACGSGGGCCGCAAGGCGGTGAGCATGTGGTTTAATTCGAAGCAACGGAAGAAC	960
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Db	961	TTACCTACTCTTGATCATCCAGAAACATTGGAGATACAGATGGTCCCTCCGGAAACTGT	1020
Gy	1021	GAGACAGGTGCTGCATGGCTGTGCTCAAGCTCGTGTGTGAATATTTGGGTTAAGTCCCGT	1080
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Gy	1201	GGGCTTACACACGTGCTCAATGGCGTATACAGAGGGCTGCAAAGTTAGCGATAGTAGACGA	1260
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Gy	1261	ATCCCAACAAAGTAGCTGTAATCCCGAATGGAGATCGCAACTCGACTCCATCAATGTCGGA	1320
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Gy	1321	ATGCTAGTAAATCGTGAATCAGAAATGTCACGGTGAATACGTTCCCGGACTTGTTCACAC	1380
Db	1321	ATGCTAGTAAATCGTGAATCAGAAATGTCACGGTGAATACGTTCCCGGACTTGTTCACAC	1380
Gy	1381	CGCCGCTCACACATGAGGAGTGAATGCTCCAAAGTAGCTAAGCTTAAACCTTCGGGAGT	1440
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Gy	1441	GAGGAGTACACAGGAGTGGTCAATGAATGGAGGTTGAAGTCATACGCG	1486
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VERSION	AF468256.1						
KEYWORDS							
SOURCE		uncultured bacterium					
ORGANISM		Bacteria; environmental samples.					
REFERENCE		1 (bases 1 to 1421)					
AUTHORS		Brinkmeyer, R. and Helmke, B.					
TITLE		Evidence for methylotrophic processes in Arctic pack ice					
JOURNAL		Unpublished					
REFERENCE		2 (bases 1 to 1421)					
AUTHORS		Brinkmeyer, R. and Helmke, B.					
TITLE		Direct Submision					
JOURNAL		Submitted (14-JAN-2002) Palagic Oceanography,					

Query Match 94.3%; Score 1400.8; DB 1; Length 1421.

Best Local Similarity 99.2%; Pred. No. 0;
Matches 1408; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

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DB 362 GAAGAAGGCTTAGGGTTGTAAGCACTTCAAGGGGTGAGGGAAGGTGATAGGTTATAC 421
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RESULT 4
AF468385
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DEFINITION Arctic sea ice bacterium ARK10032 16S ribosomal RNA gene, partial
sequence.
ACCESSION AF468385
VERSION AF468385.1 GI:28269033
KEYWORDS SOURCE
ORGANISM Arctic sea ice bacterium ARK10032
Arctic sea ice bacterium ARK10032
Bacteria; Proteobacteria; Gammaproteobacteria; Oceanospirillales;
Madinomonas.
REFERENCE 1 (bases 1 to 1425)
AUTHORS Brinkmeyer, R., and Helmke, E.
TITLE Diversity of bacteria in Arctic sea ice
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1425)
AUTHORS Brinkmeyer, R., and Helmke, E.
TITLE Direct Submission
JOURNAL Submitted (15-JAN-2002) Pelagic Oceanography,
Alfred-Wegener-Institut fuer Polar und Meeresforschung, Am
Handels Hafen 12, Bremerhaven D-27570, Germany
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Best Local Similarity 98.9%; Pred. No. 0;
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 SOURCE
 ORGANISM
Marinomonas protea
Marinomonas protea
Bacteria; Proteobacteria; Gammaproteobacteria; Oceanospirillales;
Marinomonas

REFERENCE
 AUTHORS Gilbert, J. A., Laybourn-Parry, J., Hill, P. J., and Dodd, C.
 TITLE Novel bacterial strains from Antarctic lakes
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1372)
 AUTHORS Gilbert, J. A., Laybourn-Parry, J., Hill, P. J., and Dodd, C.
 TITLE Direct Submission
 Submitted (27-MAR-2002) Life and Environmental Science, University
 of Nottingham, Sutton Bonington Campus, Sutton Bonington, Leics
 JOURNAL LE12 5RD, England

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 Marinomonas primoryensis
 Bacteria; Proteobacteria; Gammaproteobacteria; Oceanospirillales;
 Marinomonas.
 REFERENCE
 1 Romanenko, L.A., Uchino, M., Mikhailov, V.V., Zhukova, N.V. and Uchimura, T.
 Marinomonas primoryensis sp. nov., a novel psychrophile isolated from coastal sea ice in the Sea of Japan
 Int. J. Syst. Evol. Microbiol. 53, 829-832 (2003)
 2 (bases 1 to 1449)
 Uchino, M., Uchimura, T. and Romanenko, L.A.
 Direct Submission
 Submitted (12-NOV-2001) Masataka Uchino, Tokyo University of Agriculture, Department of Applied Biology and Chemistry, Sakuragaoka 1-1-1, Setagaya-ku, Tokyo 158-8502, Japan
 (E-mail: muchino@nodai.ac.jp, Tel: 81-3-5477-2324, Fax: 81-3-5477-2619)
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ACCESSION AB074193
VERSION AB074193.1 GI:18143646
KEYWORDS

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 REFERENCES
 Eilers, R., Pernthaler, J., Glockner, F. O. and Amann, R.
 Culturable and in situ abundance of pelagic bacteria from the

North Sea
 Appl. Environ. Microbiol. 66 (7), 3044-3051 (2000)
 MEDLINE
 20336458
 PUBMED
 10877804
 REFERENCES
 2 (bases 1 to 1448)
 AUTHORS
 Eilers, R.
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 DB 661 AGTGGCAAGCGACACCTTGATTAATGACACTGAGGTGGAAAGCGTGGGAGCA 720
 QY 763 AACAGATTAAATACCTGTGTATGCCAGCGGTAAGAGATGTACTAGCCGTTGGGTTG 822

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RESULT 9
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LOCUS
DEFINITION Marine Bacterium Tw-9 16S ribosomal RNA gene, partial sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

marine bacterium Tw-9
Bacteria; Proteobacteria; Gammaproteobacteria; Oceanospirillales;
Halomonadaceae.
1 (bases 1 to 1455)
Bidle, K.D. and Azam, F.
Bacterial control of silicon regeneration from diatom detritus:
significance of bacterial ectohydrolases and species identity
Limnol. Oceanogr. 46 (7), 1606-1623 (2001)
2 (bases 1 to 1455)
Bidle, K.D. and Azam, F.
Direct Submission
Submitted (01-MAR-2001) Scripps Institution of Oceanography,
University of California San Diego, 9500 Gilman Drive, La Jolla, CA
92093-0202, USA

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BASE COUNT 372 a 320 c 453 g 310 t
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Db 720 GACACTGAGTGCAGAAAGGTGGGAGCAACAGATTAATGATACCTGTGTAGCG 779
Qy 794 GTAACGATGTCTACTAGCCGCTGGGTTGATGATAGTGGCGACCTAAGCATTA 853
Db 780 GTAACGATGTCTACTAGCCGCTGGGTTGATGATAGTGGCGACCTAAGCATTA 839
Qy 854 GTAGACCGCTGGGAGTACGGCGCAAGGTTAAATCAATGATGACGGGGCGG 913
Db 840 GTAGACCGCTGGGAGTACGGCGCAAGGTTAAATCAATGATGACGGGGCGG 899

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QY 914 CACAAGCGGTGAGCATGTGTTAATTCGAGCAACGCAAGAACCTTACTACTCTTG 973
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QY 974 ACATCCACAGAACATTTGAGAGATCAGATGTGCTTCGGGAACCTGAGACAGGTGCTG 1033
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Db 1438 GAGTGTCA 1447

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LOCUS Marimonas mediterranea strain MMB-1.16S ribosomal RNA gene,
DEFINITION complete sequence.
ACCESSION AF063027
VERSION AF063027.1 GI:3929025
KEYWORDS Marimonas mediterranea
SOURCE Marimonas mediterranea
ORGANISM Bacteria; Proteobacteria; Gammaproteobacteria; Oceanospirillales;
Marimonas.
REFERENCE 1 (bases 1 to 1534)
AUTHORS Solano, F. and Sanchez-Amat, A.
TITLES Studies on the phylogenetic relationships of melanogenic marine
bacteria: proposal of Marimonas mediterranea sp. nov
JOURNAL Int. J. Syst. Bacteriol. 49 Pt 3, 1241-1246 (1999)
MEDLINE 9934518
PubMed 10425786
REFERENCE 2 (bases 1 to 1534)
AUTHORS Sanchez-Amat, A. and Solano, F.
TITLES Direct Submission
JOURNAL Submitted (04-MAY-1998) Genetics and Microbiology, Faculty of
Biology, University of Murcia, Campus de Espinardo, Murcia 30100,
Spain
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QY 181 GGGGACTCTTCGAGACCTTCGCTTAAATGATGAGCTGCTGATGATTACTGTTGCTG 240
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QY 541 AATTACTGGGCGTAAACGCGCGTAGGTGTTGTTAAGTCGATGTGAATCCAGGCG 600
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LOCUS AX175616
DEFINITION Sequence 4 from Patent WO0144275.
ACCESSION AX175616
VERSION AX175616.1 GI:14589835
KEYWORDS
SOURCE
ORGANISM
Marinomonas communis
Marinomonas communis
Bacteria; Proteobacteria; Gammaproteobacteria; Oceanospirillales;
Marinomonas.

REFERENCE
AUTHORS
1 Berry, M.J., Griffiths, A.U., Hill, P.J., Laybourne-Parry, J. and
Mills, S.V.
TITLE Processes and organisms for the production of anti-freeze proteins
JOURNAL Patent: WO 0144275-A 4 21-JUN-2001;
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Best Local Similarity 93.7%; Pred. No. 0;
Matches 1374; Conservative 1; Mismatches 83; Indels 9; Gaps 7;

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Qy 181 GGGAGCTTTCGAGCGCTTCGGCTATTGATGAGCGTGGGAGATTGCTAGTGGTAG 240

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LOCUS AF321017

DEFINITION Marinomonas sp. GOBB3-320 16S ribosomal RNA gene, partial sequence.

ACCESSION AF321017

VERSION AF321017.2 GI:30159656

KEYWORDS

SOURCE Marinomonas sp. GOBB3-320

ORGANISM Marinomonas sp. GOBB3-320

Bacteria; Proteobacteria; Gammaproteobacteria; Oceanospirillales; Marinomonas.

REFERENCE 1 (bases 1 to 1343)

AUTHORS Kisanand, V., Cuadros, R. and Wikner, J.

TITLE Phylogeny of culturable estuarine bacteria catbolizing riverine organic matter in the northern Baltic Sea

JOURNAL Appl. Environ. Microbiol. 68 (1), 379-388 (2002)

MEDLINE 21633837

PUBMED 11772648

REFERENCE 2 (bases 1 to 1343)

AUTHORS Kisanand, V., Cuadros, R. and Wikner, J.

TITLE Direct Submission

JOURNAL Submitted (11-NOV-2000) Department of Microbiology, University of Umea, Umea S-90187, Sweden

REFERENCE 3 (bases 1 to 1343)

AUTHORS Kisanand, V., Cuadros, R. and Wikner, J.

TITLE Direct Submission

JOURNAL Submitted (28-APR-2003) Department of Microbiology, University of Umea, Umea S-90187, Sweden

REMARK Nucleotide sequence updated by submitter

COMMENT On Apr 28, 2003 this sequence version replaced gi:13336278.

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ORIGIN

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Best Local Similarity 95.1%; Pred. No. 0;

Matches 1279; Conservative 0; Mismatches 62; Indels 4; Gaps 4;

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QY 194 AGCTTCGCGTATTAAGTGAAGCTGCGTGAAGTATGCTAGTGAAGGTAAGGCTAC 253

Db 121 AGCTTCGCGTATTAAGTGAAGCTGCGTGAAGTATGCTAGTGAAGGTAAGGCTAC 180

QY 254 CAAGCGAGCATCTTAAGTGTCTGAGAGAGTACCACTCACTGGAGTGAACAG 313

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QY 314 GCCGAGACTCTTACGGGAGGACAGATGGGGAATATTGGACATGGCGCAAGCTGATC 373

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QY 374 CAGCCATGGCGGTGTGGAAGAAAGGCTTGGGTTGAAAGCACTTCAGGGGTGAGA 433

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QY 674 TGAATGCGTATATTAAGAAAGAAATCATAGTGGGAAAGGACACCTTGACTAATACT 733

Db 601 TGAATGCGTATATTAAGAAAGAAATCATAGTGGGAAAGGACACCTTGACTAATACT 659

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QY 794 GTAACGATGTCT-ACTAGCGGTGGTGTGTTAATGACTTAAGTGG-CCGAGCTAACGAAT 851

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VERSION 16S-like rRNA.
KEYWORDS Marinomonas vaga
SOURCE Marinomonas vaga
ORGANISM Bacteria; Proteobacteria; Gammaproteobacteria; Oceanospirillales; Marinomonas.
REFERENCE 1 (bases 1 to 1467)
AUTHORS Gauthier M.J., Lafay, B., Christen, R., Fernandez, L., Acquaviva, M., Bonin, P. and Bertrand, J.C.
TITLE Marinobacter hydrocarbonoclasticus gen. nov., sp. nov., a new, extremely halotolerant, hydrocarbon-degrading marine bacterium
JOURNAL Int. J. Syst. Bacteriol. 42 (4), 568-576 (1992)
MEDLINE 93002312
REFERENCE 2
AUTHORS Lafay, B.
TITLE Direct Submission
JOURNAL Submitted (17-JUN-1992) B. Lafay, URA 671 CNRS-Universite Paris VI, Station Zoologique, Villefranche-sur-Mer, 06230, FRANCE
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VERSION AF468267.1 GI:28268916
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SOURCE uncultured bacterium
ORGANISM Bacteria; environmental samples.
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AUTHORS Brinkmeyer R. and Helmke, E.
TITLE Evidence for methylo trophic processes in Arctic pack ice
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1417)
AUTHORS Brinkmeyer R. and Helmke, E.
TITLE Direct Submission
JOURNAL Submitted (14-JAN-2002) Pelagic Oceanography,
Alfred-Wegener-Institut fuer Polar und Meeresforschung, Am
Handelskafen 12, Bremerhaven D-27570, Germany
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Job time : 5677.5 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 30, 2004, 08:32:25 ; Search time 438.94 Seconds
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Title: US-09-737-297-1

Perfect score: 1486

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Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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9	1131	76.1	1501	AA166302
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11	1126.2	75.8	1480	AA150855
12	1121.4	75.5	1480	AA150856
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15	1100.2	74.0	1467	AAH11023
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17	1096	73.8	1528	AAH83570
18	1089.4	73.3	1450	AAV36877
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ALIGNMENTS

RESULT 1

AAH25691 standard; DNA; 1485 BP.

AC AAH25691:

XX 05-SEP-2001 (first entry)

XX Nucleotide sequence of 16S rRNA of *Marinomonas protea*.

DE Nucleotide sequence of 16S rRNA of *Marinomonas protea*.

KW 16S rRNA; anti-freeze protein; food additive; frozen vegetable;

KM frozen confectionery; ss.

XX

OS *Marinomonas protea*.

XX

XX WO200144275-A2.

XX 21-JUN-2001.

XX

XX 05-DEC-2000; 2000WO-BP12396.

XX

XX 15-DEC-1999; 99GB-0029696.

XX

XX (UNITL) UNILEVER PLC.

XX (UNITL) UNILEVER NV.

XX (HIND-) HINDUSTAN LEVER LTD.

XX

XX Berry M., Griffiths A., Hill PJ, Laybourne-Parry J, Mille SV,

XX WPI, 2001-398120/42.

XX

PT Preparing anti-freeze peptides useful in frozen food products, e.g.
 CC frozen vegetables and confectionery, by culturing bacteria from aqueous
 PT low-temperature environment and extracting anti-freeze proteins from
 PT culture -

XX Claim 2, Page 55, 59pp; English.

CC The present sequence represents the 16S rRNA of Marinomonas protea.
 CC Anti-freeze proteins can be isolated from M. protea, using the method
 CC of the invention. The specification describes a method for producing
 CC anti-freeze peptides (AFPs). The method comprises collecting one or
 CC more samples of bacteria from an aqueous low-temperature environment,
 CC culturing the bacteria and extracting proteins from the samples, testing
 CC the proteins for anti-freeze properties, selecting proteins having
 CC anti-freeze properties and producing the selected protein for use as
 CC an AFP food additive. The method is useful for producing AFPs which are
 CC incorporated in food products, such as frozen vegetables and frozen
 CC confectionery such as ice-cream. AFPs are useful in frozen food products,
 CC such as vegetables, soups, snacks, dairy products and frozen
 CC confectionery, which includes sorbet, water-ice, granites, frozen fruit
 CC purees and milk-containing frozen products such as ice-cream, frozen
 CC yogurt or custards, sherbet and ice-milk.

XX Sequence 1485 BP; 383 A; 325 C; 465 G; 312 T; 0 other;

Query Match 99.2%; Score 1474; DB 22; Length 1485;

Best Local Similarity 99.9%; Pred. No. 0; Mismatches 0; Indels 1; Gaps 1;

Matches 1485; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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 DB 242 GGTAAAGGCTTACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300
 QY 301 GGAAGTGAACACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
 DB 301 GGAAGTGAACACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
 QY 361 GGAAGTGAACACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
 DB 361 GGAAGTGAACACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
 QY 421 TCAGGGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480
 DB 421 TCAGGGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480
 QY 481 AGCAGCGGCTAATCTGTGCGCAGCAGCGCGGTAAATACAGGGGTGAAGCGTTAATCG 540
 DB 481 AGCAGCGGCTAATCTGTGCGCAGCAGCGCGGTAAATACAGGGGTGAAGCGTTAATCG 540
 QY 541 AATTACTGGGCTTAAAGGCGCGGTAGTGTGTTGTTAAGTCGATGTAATCCAGGCG 600
 DB 541 AATTACTGGGCTTAAAGGCGCGGTAGTGTGTTGTTAAGTCGATGTAATCCAGGCG 600
 QY 601 TCAACTTGAATGACCCGATGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAG 660
 DB 601 TCAACTTGAATGACCCGATGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAG 660

QY 661 TCCTGTGTAGCGGTGAATGCGTAGATATAGGAGGAGGAGGAGGAGGAGGAGGAGG 720
 DB 661 TCCTGTGTAGCGGTGAATGCGTAGATATAGGAGGAGGAGGAGGAGGAGGAGGAGG 720
 QY 721 CTGAGCTAATAGTGAACATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
 DB 721 CTGAGCTAATAGTGAACATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
 QY 781 GGTAGTCCAGCGCGTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
 DB 781 GGTAGTCCAGCGCGTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
 QY 841 GCTAAGGCAATAGTGAACATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 900
 DB 841 GCTAAGGCAATAGTGAACATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 900
 QY 901 TGAAGGGGGCGCCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 960
 DB 901 TGAAGGGGGCGCCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 960
 QY 961 TTAAGTCTTGAATGAGTGAACATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1020
 DB 961 TTAAGTCTTGAATGAGTGAACATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1020
 QY 1021 GAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1080
 DB 1021 GAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1080
 QY 1081 AACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1140
 DB 1081 AACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1140
 QY 1141 GCGGGTGAACAAACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1200
 DB 1141 GCGGGTGAACAAACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1200
 QY 1201 GGGGCTACACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1260
 DB 1201 GGGGCTACACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1260
 QY 1261 ATCCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1320
 DB 1261 ATCCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1320
 QY 1321 ATGCTAGTATGCTGATGAGTGAATGAGTGAATGAGTGAATGAGTGAATGAGTGA 1380
 DB 1321 ATGCTAGTATGCTGATGAGTGAATGAGTGAATGAGTGAATGAGTGAATGAGTGA 1380
 QY 1381 GCGCCGTCACACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1440
 DB 1381 GCGCCGTCACACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1440
 QY 1441 GCGCGTGAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1485
 DB 1441 GCGCGTGAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1485

RESULT 2
 ID AA164997
 AA164997 standard; DNA; 1501 BP.
 AC AA164997;
 XX
 DT 11-DEC-2001 (first entry)
 XX
 DE Polyhydroxyalkanoic acid related Pseudomonas jessenii coding sequence.
 XX
 KW Polyhydroxyalkanoic acid; PHA; functional polymer; ds.
 XX
 OS Pseudomonas jessenii.
 XX
 FN JP2001178486-A.
 XX

PD 03-JUL-2001.
 XX 27-DEC-1999; 99JP-0371870.
 XX 27-DEC-1999; 99JP-0371870.
 PR
 XX (CANO) CANON KK.
 XX
 DR WPI; 2001-592590/67.
 XX
 PT Production of a polyhydroxyalkanoate useful as a functional polymer -
 XX
 PS Disclosure; Page 7-8; 10pp; Japanese.
 XX
 CC The present invention relates to a method for the production of
 CC polyhydroxyalkanoic acid (PHA). This can be used as a functional polymer.
 CC The present sequence is a pseudomonas jessenii coding sequence which was
 CC described in the exemplification of the invention.
 XX
 SQ Sequence 1501 BP; 379 A; 339 C; 475 G; 308 T; 0 other;

Query Match 76.1%; Score 1131; DB 22; Length 1501;
 Best Local Similarity 88.2%; Pred. No. 0;
 Matches 1299; Conservative 0; Mismatches 165; Indels 9; Gaps 6;

QY 13 TGAACGCTGGCGGAGGCTTAAACATGCAAGTCGAGCGGTACAGGCGAGCTTGCTCC 72
 DB 1 TGAACGCTGGCGGAGGCTTAAACATGCAAGTCGAGCGGTACAGGCGAGCTTGCTCC 58
 QY 73 TGTCTACGAGCGCGGAGCGGTGATGACCGCTGAGGATCTGCTTATGTAAGGGGACAA 132
 DB 59 TGAATTC-AGCGGCGGAGCGGTGATGATGCTAGGAAATCTGCTGTAATGAGGACAA 117
 QY 133 CAGTGGGAAACGCGATCTAATACCGCATCGGCTGAGGCGGAAAGAGGAGGACTCTTCG 192
 DB 118 CGTCTGAAAGGAGCGCTAATACCGCATCGGCTGAGGCGGAAAGAGGAGGACTCTTCG 175
 QY 193 GAGCCTTCGCTATTAGATGAGCGCTGAGATTAGCTAGTTGGTAGGGTAAAGCCTTA 252
 DB 176 GGGCTTGGCGCTATCAGATGAGCGCTAGTGGATTAGCTAGTTGGTAGGGTAAAGCCTTA 235
 QY 253 CCAAGGCGAGATCTCTAATGCTGTCGAGAGATGACAGTACACTGGGACTAGACAC 312
 DB 236 CCAAGGCGAGATCTCTAATGCTGTCGAGAGATGATGATCACTGAACTGAGAAC 295
 QY 313 GGCCAGACTCTCTACCGGAGGAGCAGCAGTGGGAAATATGACATGGGCGGAGCTGAT 372
 DB 296 GGTCCAGACTCTCTACCGGAGGAGCAGCAGTGGGAAATATGACATGGGCGGAGCTGAT 355
 QY 373 CCAAGCATTGCGGCTGTGTGAGAGAGGCTTAGGGTGTAAAGCACTTCAGGGGTAGG 432
 DB 356 CCAAGCATTGCGGCTGTGTGAGAGAGGCTTAGGGTGTAAAGCACTTCAGGGGTAGG 415
 QY 433 AAGGGTATGATGTTAATACCTTATCTTGAAGTGAAGCCGAGAAAGACACCGCTTA 492
 DB 416 AAGGGTATGATGTTAATACCTTATCTTGAAGTGAAGCCGAGAAAGACACCGCTTA 475
 QY 493 CTCTGTGCGAGCAGCGCGGTAAATACAGAGGGTGAAGGCTTAATCGAATTTACTGGGCG 552
 DB 476 CTCTGTGCGAGCAGCGCGGTAAATACAGAGGGTGAAGGCTTAATCGAATTTACTGGGCG 535
 QY 553 TAAAGCGCGGTAGGTGTTGTTAAGTCGAAATGCCAGGGCTCAACCTTGGA 612
 DB 536 TAAAGCGCGGTAGGTGTTGTTAAGTCGAAATGCCAGGGCTCAACCTTGGA 595
 QY 613 TGGCACCAGTACTGCTAGCTAGATGATGTAAGAGGGGTGGAATTTCTGTGTACG 672
 DB 596 CTGATCTCAAACTGCAAGCTAGATGTAAGAGGGGTGGAATTTCTGTGTACG 655
 QY 673 GTGAATGCGTAGTATAGGAAGAACATCAGTGGGAGGCGACACCTGGACTAATAC 732
 DB 656 GTGAATGCGTAGTATAGGAAGAACATCAGTGGGAGGCGACACCTGGACTAATAC 715

QY 733 TGAACCTGAGTGGCGAAGGCGGAGCAACAGATTAAGTACCTCGTAGTCCAGC 792
 DB 716 TGAACCTGAGTGGCGAAGGCGGAGCAACAGATTAAGTACCTCGTAGTCCAGC 775
 QY 793 CGTAAACGATGTCTAATGAGCGTTGG--GTTGTAATGACTTATGAGCGGAGCTAACGAA 850
 DB 776 CGTAAACGATGTCTAATGAGCGTTGGAGCTTGAAGCTTATGAGCGGAGCTAACGAT 835
 QY 851 TAAGTAGACCGCTGGGAGATACCGCGGAGGTTAAATCTCAATATGAGGAGGCG 910
 DB 836 TAAGTAGACCGCTGGGAGATACCGCGGAGGTTAAATCTCAATATGAGGAGGCG 895
 QY 911 CCGCACAAGCGGTGAGCATGTGTTTATTCGAAGCAACGGAAGACCTTACTACTC 970
 DB 896 CCGCACAAGCGGTGAGCATGTGTTTATTCGAAGCAACGGAAGACCTTACTACTC 955
 QY 971 TTGACATCCACGAACATTTGAGAGATGATGTTGCTTGGGAACTGTGACACAGTG 1030
 DB 956 TTGACATCCACGAACATTTGAGAGATGATGTTGCTTGGGAACTGTGACACAGTG 1015
 QY 1031 CTGATGAGCTGTGTCAGCTGCTGTTGAAATGTTGAGTTAAGTCCGTTACGAGGCA 1090
 DB 1016 CTGATGAGCTGTGTCAGCTGCTGTTGAAATGTTGAGTTAAGTCCGTTACGAGGCA 1075
 QY 1091 ACCCTTGTCTTATTGTCAGCAGCATTAATGTTGAGTTAAGTCCGTTACGAGGCA 1150
 DB 1076 ACCCTTGTCTTATTGTCAGCAGCATTAATGTTGAGTTAAGTCCGTTACGAGGCA 1135
 QY 1151 AACCGAAGAAAGTGGGAGCAGCATGATCATATGAGTCCGTTACGAGTGGGCTAGACA 1210
 DB 1136 AACCGAAGAAAGTGGGAGCAGCATGATCATATGAGTCCGTTACGAGTGGGCTAGACA 1195
 QY 1211 CGTGTCAATATGCTTATACAGAGGCTGCAAGCTAGAGATGATGAGCGAATCCACAAA 1270
 DB 1196 CGTGTCAATATGCTTATACAGAGGCTGCAAGCTAGAGATGATGAGCGAATCCACAAA 1255
 QY 1271 GTACGTGTGATGTCGAGATTTGAGAGTGTGCAATCTGATCTCAATGAGTGGGATGCTAGTA 1330
 DB 1256 ACCGATGCTGATGTCGAGATTTGAGAGTGTGCAATCTGATCTCAATGAGTGGGATGCTAGTA 1315
 QY 1331 ATCGTAATCAGATGTCAGGATGATGCTTCCGAGGCTTGTACACACCGCGCTCAC 1390
 DB 1316 ATCGTAATCAGATGTCAGGATGATGCTTCCGAGGCTTGTACACACCGCGCTCAC 1375
 QY 1391 ACCATGAGATGATGCTTCCAGAAATGATGCTTAACTCTTGGGAGTGGCGTTACC 1450
 DB 1376 ACCATGAGATGATGCTTCCAGAAATGATGCTTAACTCTTGGGAGTGGCGTTACC 1433
 QY 1451 ACGGATGCTCAATGACTGGGTTGAAGTCTAC 1483
 DB 1434 ACGGATGCTCAATGACTGGGTTGAAGTCTAC 1466

RESULT 3
 AA164998
 ID AA164998 standard; DNA; 1501 BP.

XX AA164998;
 XX
 DT 11-DEC-2001 (first entry)
 XX
 DE Polyhydroxyalkanoic acid related Pseudomonas jessenii coding sequence.
 XX
 KW Polyhydroxyalkanoic acid; PHA; biodegradable plastic; ds.
 XX
 OS Pseudomonas jessenii.
 XX
 PN JP2001178484-A.
 XX
 PD 03-JUL-2001.
 XX
 PF 27-DEC-1999; 99JP-0371866.
 XX

XX WPI; 2001-586288/66.
 XX
 PT Production of a polyhydroxyalkanoate useful as a functional polymer -
 XX
 PS Disclosure, Page 9, 12pp; Japanese.
 XX
 CC The present invention describes a method of producing a
 CC polyhydroxyalkanoate (PHA) using a microbe. This may be *Pseudomonas*
 CC *cichorii* YN2, *Pseudomonas cichorii* H45 or *Pseudomonas jessenii* P161. The
 CC PHA produced using the method of the invention is useful as a functional
 CC polymer. The present sequence is a fragment of the P. jessenii coding
 CC sequence.
 XX
 SQ Sequence 1501 BP; 379 A; 339 C; 475 G; 308 T; 0 other;
 Query Match 76.1%; Score 1131; DB 22; Length 1501;
 Best Local Similarity 88.2%; Pred. No. 0; Mismatches 165; Indels 9; Gaps 6;
 Matches 1299; Conservative 0;
 QY 13 TGAACGCTGGCGGCGAGGCTTAAACATGCAAGTCGAGCGGTAAACAGGGGAGCTTGCTCC 72
 Db 1 TGAACGCTGGCGGCGAGGCTTAAACATGCAAGTCGAGCGG-ATGACGCGAGCTTGCTCC 58
 QY 73 TGTCTGACGAGCGCGGAGCGGTGAGTAAACGCGTAGGAATCTGCTAGTAGAGGGGACAA 132
 Db 59 TGAATTC-AGCGCGGAGCGGTGAGTAAATGCTTAGGAATCTGCTGAGTAGGGGACAA 117
 QY 133 CATGTGGAACGCAATCTATACCGCATACGCGCTGAGGGGAAAGAGGGGAGCTTTCG 192
 Db 118 CGTCTGMAAAGGAGACGCTAATACCGCATACGCGCTGAGGGGAAAGAGGGGAGCTTTCG 175
 QY 193 GAGCCTTCGCTATTAGATGAGCTTGCCTGAGATTAGCTAGTTGGTAGGGTAAAGGCTTA 252
 Db 176 GGGCCTTGGCGCTATCAGATGAGCTTGCCTGAGATTAGCTAGTTGGTAGGGTAAAGGCTTA 235
 QY 253 CCAAGGCGAGCATCTCTATCTGTCGAGAGGATGACAGTCAACATCGGCTAGAGCAC 312
 Db 236 CCAAGGCGAGCATCTCTATCTGTCGAGAGGATGACAGTCAACATCGGCTAGAGCAC 295
 QY 313 GGGCCAGACTCTCTATCTGTCGAGAGGATGACAGTCAACATCGGCTAGAGCAC 372
 Db 296 GGTCCAGACTCTCTATCTGTCGAGAGGATGACAGTCAACATCGGCTAGAGCAC 355
 QY 373 CCAAGCCTTCGCTATTAGATGAGCTTGCCTGAGATTAGCTAGTTGGTAGGGTAAAGGCTTA 432
 Db 356 CCAAGCCTTCGCTATTAGATGAGCTTGCCTGAGATTAGCTAGTTGGTAGGGTAAAGGCTTA 415
 QY 433 AAGGCTGATAGTTAATATGATCTTGAAGTTCGCTTGAAGTTCGCTTGAAGTTCGCTTGA 492
 Db 416 AAGGCTGATAGTTAATATGATCTTGAAGTTCGCTTGAAGTTCGCTTGAAGTTCGCTTGA 475
 QY 493 CTCTGTGCGAGCAGCGCGGTAAATACAGAGGTCGAGCGGTAAATCGGATTTACTGAGCG 552
 Db 476 CTCTGTGCGAGCAGCGCGGTAAATACAGAGGTCGAGCGGTAAATCGGATTTACTGAGCG 535
 QY 553 TAAAGGCGCGGTAAATACAGAGGTCGAGCGGTAAATCGGATTTACTGAGCG 612
 Db 536 TAAAGGCGCGGTAAATACAGAGGTCGAGCGGTAAATCGGATTTACTGAGCG 595
 QY 613 TGGACCCGATATCTGCTAGCTAGATAGTAGAGGAGGAGTTCGCTTGAAGTTCGCTTGA 672
 Db 596 CTGCTATTCATAAATCTGAGCTAGATAGTAGAGGAGGAGTTCGCTTGAAGTTCGCTTGA 655
 QY 673 GTGAATTCGCTAGATATAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 732
 Db 656 GTGAATTCGCTAGATATAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 715
 QY 733 TGAACCTGAGTTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 792
 Db 716 TGAACCTGAGTTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 775
 QY 793 CGTAAACGATGTCTACTAGCCGTTGG--GTGTAATGACTTAGTGGCGGAGCTAACGCA 850

Db 776 CGTAAACGATGTCTACTAGCCGTTGGAGGCTTGAAGTTCGCTTGAAGTTCGCTTGAAG 835
 QY 851 TGAATTCGCTAGATATAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 910
 Db 836 TGAATTCGCTAGATATAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 895
 QY 911 CGGACCAAGCGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 970
 Db 896 CGGACCAAGCGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 955
 QY 971 TGAATTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1030
 Db 956 TGAATTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1015
 QY 1031 CTGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1090
 Db 1016 CTGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1075
 QY 1091 ACCCTTGTCTTATTTGCGAGCAGCTAATGCTGAGGAGGAGGAGGAGGAGGAGGAGG 1150
 Db 1076 ACCCTTGTCTTATTTGCGAGCAGCTAATGCTGAGGAGGAGGAGGAGGAGGAGGAGG 1135
 QY 1151 AACCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1210
 Db 1136 AACCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1195
 QY 1211 CGTGTACATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1270
 Db 1196 CGTGTACATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1255
 QY 1271 GTAGCTGAGTTCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1330
 Db 1256 ACCGATGCTAGTTCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1315
 QY 1331 ATCTGATACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1390
 Db 1316 ATCTGATACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1375
 QY 1391 ACCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1450
 Db 1376 ACCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1433
 QY 1451 ACCGATGCTAGTTCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1483
 Db 1434 ACCGATGCTAGTTCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1466
 RESULT 5
 AS12097
 ID AS12097 standard; DNA; 1501 BP.
 XX
 AC AS12097;
 XX
 DT 21-NOV-2001 (first entry)
 XX
 DE *Pseudomonas jessenii* 161 strain.
 XX
 KW Polyhydroxyalkanoate; alkanoate; microorganism; functional polymer; ds;
 KM medical material.
 OS *Pseudomonas jessenii*.
 XX
 PN EP1113033-A2.
 XX
 PD 04-UTL-2001.
 XX
 PF 22-DEC-2000; 2000EP-0128444.
 XX
 PR 27-DEC-1999; 99JP-0371863.
 PR 31-JAN-2000; 2000JP-0023078.
 PR 31-JAN-2000; 2000JP-0023080.
 PR 31-JAN-2000; 2000JP-0023083.

PR 30-MAR-2000; 2000JP-0095011.
 PR 30-MAR-2000; 2000JP-0095012.
 PR 30-MAR-2000; 2000JP-0095013.
 PR 07-JUL-2000; 2000JP-0207089.
 PR 07-JUL-2000; 2000JP-0207091.
 PR 27-NOV-2000; 2000JP-0359789.
 XX
 PA (CANO) CANON KK.
 PI Honna T, Kobayashi T, Yano T, Kobayashi S, Inamura T, Suda S,
 PI Kenmoku T,
 DR WPI; 2001-537748/60.
 XX
 PT New polyhydroxyalkanoates useful as functional polymers e.g. in medical
 PT devices
 XX
 PS Claim 36; Page 83-84; 184pp; English.
 XX
 CC The invention relates to polyhydroxyalkanoates comprising monomer units
 CC of diverse structures containing side chain substituents. This sequence
 CC represents a Pseudomonas jessenii 161 strain microorganism, capable of
 CC synthesising a polyhydroxyalkanoate from an alkanoate. By culturing a
 CC microorganism in a medium containing an alkanoate, a polyhydroxyalkanoate
 CC can be obtained. Polyhydroxyalkanoates are used as functional polymers,
 CC particularly in medical devices and materials. The use of microorganisms
 CC yields polymers of high purity and in high yield.
 XX
 SQ Sequence 1501 BP; 379 A; 339 C; 475 G; 308 T; 0 other;
 Query Match 76.1%; Score 1131; DB 22; Length 1501;
 Best Local Similarity 88.2%; Pred. No. 0;
 Matches 1259; Conservative 0; Mismatches 165; Indels 9; Gaps 6;

QY 13 TGAACCTGCGCGGCAAGCTTAAACACATGACATGACGCGGTAAACAGGGAGCTTGCTC 72
 Db 1 TGAACCTGCGCGGCAAGCTTAAACACATGACATGACGCGGTAAACAGGGAGCTTGCTC 58
 QY 73 TCGTACGAGCGCGGAGCGGTGAGTAAACGCGTAAAGATCTGCTAGTAAAGGGACAA 132
 Db 59 TGAATTC-AGCGGCGGAGCGGTGAGTAAAGTAAAGTCTGCTAGTAAAGGGACAA 117
 QY 133 CATGTGAAAGCAGATGCTAAATCCGCAATACCGCTGAGGGGAAAGAGGGGACTCTTCG 192
 Db 118 GGTCTGAAAGGAGGAGCTTAATCCGCAATACCGCTGAGGGGAAAGAGGGGACTCTTCG 175
 QY 193 GAGCTTCCGCTATTAGATGAGCTGCGTGAATGATGATGATGATGATGATGATGATGAT 252
 Db 176 GGGCTTGGCTATCAGATGAGCTGAGTGGATGATGATGATGATGATGATGATGATGAT 235
 QY 253 CCAAGCGGAGATCTCTTAATCTGTGAGAGAGTAAACATGACATGAGGAGTAAAGGCTCA 312
 Db 236 CCAAGCGGAGATCTCTTAATCTGTGAGAGAGTAAACATGACATGAGGAGTAAAGGCTCA 295
 QY 313 GGGCCAGACTCTCTTACGAGGAGGAGCAGTGGGAAATATTGACATGAGGAGGAGGAGGCTGAT 372
 Db 296 GGTCCAGACTCTCTTACGAGGAGGAGCAGTGGGAAATATTGACATGAGGAGGAGGAGGCTGAT 355
 QY 373 CCAAGCGGAGCTGCTGTGTGAGAGAGGCTTAAAGCTTAAAGCTTAAAGGAGGAGGCTGAT 432
 Db 356 CCAAGCGGAGCTGCTGTGTGAGAGAGGCTTAAAGCTTAAAGCTTAAAGGAGGAGGCTGAT 415
 QY 433 AAGGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 492
 Db 416 AAGGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 475
 QY 493 CTCTGTGCGAGAGCGCGGCTTAATCAAGAGGCTGACAGCTTAAATCGGAATTAATCGAGGCTG 552
 Db 476 CTCTGTGCGAGAGCGCGGCTTAATCAAGAGGCTGACAGCTTAAATCGGAATTAATCGAGGCTG 535
 QY 553 TAAAGCGCGGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 612
 Db 536 TAAAGCGCGGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 595

QY 613 TGGCACCCGAGTACTGAGCTAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 672
 Db 596 CTGATTTCAAACTGAGAACCTTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 655
 QY 673 GTGAATAGCTAGATATAGAGAGAGAACATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 732
 Db 656 GTGAATAGCTAGATATAGAGAGAGAACATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 715
 QY 733 TGACATGAGGTGCGAAAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 792
 Db 716 TGACATGAGGTGCGAAAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 775
 QY 793 CGTAAACGATGCTACTAGGCGGCTTGG--GTGTAAATGACTTGTGCGGAGCTAAACGAGCA 850
 Db 776 CGTAAACGATGCTACTAGGCGGCTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 835
 QY 851 TAAATGAGCGCGCTGAGGAGGAGTACGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 910
 Db 836 TAAATGAGCGCGCTGAGGAGGAGTACGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 895
 QY 911 CCGAGAGAG 970
 Db 896 CCGAGAGAG 955
 QY 971 TTGACATCCAGAGAACATTTAGAGAGTCAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1030
 Db 956 TTGACATCCAGAGAACATTTAGAGAGTCAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1015
 QY 1031 CTGATAGGCTGTGCTGAGCTGCTGTGTGAAATGTTGGGTTAAAGTCCGTTAAACGAGGCA 1090
 Db 1016 CTGATAGGCTGTGCTGAGCTGCTGTGTGAAATGTTGGGTTAAAGTCCGTTAAACGAGGCA 1075
 QY 1091 ACCCTTGCTTATTTCCAGCAGCTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1150
 Db 1076 ACCCTTGCTTATTTCCAGCAGCTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1135
 QY 1151 AACCAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1210
 Db 1136 AACCAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1195
 QY 1211 GGTGCTCAATGAGGCTAATCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1270
 Db 1196 GGTGCTCAATGAGGCTAATCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1255
 QY 1271 GTACGTGATGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1330
 Db 1256 ACCGATGATGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1315
 QY 1331 ATCGTGAATCAAGATGCTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1390
 Db 1316 ATCGTGAATCAAGATGCTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1375
 QY 1391 ACCATGAGAGTGAATGCTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1450
 Db 1376 ACCATGAGAGTGAATGCTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1433
 QY 1451 ACGAGTGTCAATGACTGGGAGTGAAGTCTAC 1483
 Db 1434 ACGAGTGTCAATGACTGGGAGTGAAGTCTGAC 1466

RESULT 6
 AA164177
 ID AA164177 standard; DNA; 1501 BP.
 XX
 AC AA164177;
 XX
 D7 26-FEB-2002 (first entry)
 XX
 DE Pseudomonas jessenii strain Pl61 16S rRNA gene sequence.
 XX
 KM 16S rRNA gene; strain Pl61; polyhydroxyalkanoate; alkylaryl group;

KM alkanoate polymerisation; microbial enzyme; glass transition temperature;
KW adhesive; identification; ribosomal RNA; de.
XX
OS Pseudomonas jessenii.
XX
PN EPI118629-A2.
XX
PD 25-JUL-2001.
XX
PF 27-DEC-2000; 2000EP-0128540.
XX
PR 27-DEC-1999; 99UP-0371864.
XX
PR 27-DEC-1999; 99UP-0371867.
XX
PR 27-DEC-1999; 99UP-0371868.
XX
PR 27-DEC-1999; 99UP-0371869.
XX
PR 31-JAN-2000; 2000UP-0023024.
XX
PR 31-JAN-2000; 2000UP-0023025.
XX
PR 28-NOV-2000; 2000UP-0361323.
XX
PA (CANO) CANON KK.
XX
PI Honma T, Kobayashi T, Yano T, Kobayashi S, Imamura T, Suda S;
PI kemmoku T;
XX
DR WFI; 2001-598513/68.
XX
PT Polyhydroxyalkanoate comprises monomeric unit that has pendant
XX alkylaryl group, optionally substituted on benzene ring.
XX
PS Disclosure; Fig 12; 95pp; English.
XX
XX The present sequence represents that of the 16S rRNA (ribosomal RNA) gene
XX from Pseudomonas jessenii strain 161. Prior to the present invention,
XX strain 161 had not been assigned to a particular species; comparison
XX of the strain 161 16S rRNA gene DNA with 16S rRNA gene sequences of
XX known micro-organisms of the genus Pseudomonas identified 161 as a
XX strain of Pseudomonas jessenii. The specification describes a
XX polyhydroxyalkanoate comprising one or more monomeric units that have
XX pendant alkylaryl groups, optionally substituted on the benzene ring.
XX The specification also describes a process of producing the
XX polyhydroxyalkanoate by culturing a micro-organism in a medium containing
XX a raw material alkanoate and a yeast extract so that the alkanoate is
XX polymerised. The invention is used for the production of novel
XX polyalkanoates using microbial enzymes. The polymer is adhesive at
XX ambient temperatures and, when mixed with other polymers, reduces the
XX glass transition temperature of the blend. Orientation and crystallinity
XX can be tailored by changing the pendant substituent groups. The desired
XX polymer can be obtained without interference from unintended monomer
XX units.
SQ Sequence 1501 BP; 379 A; 339 C; 475 G; 308 T; 0 other:
Query Match 76.1%; Score 1131; DB 23; Length 1501;
Best Local Similarity 88.2%; Pred. No. 0;
Matches 1299; Conservative 0; Mismatches 165; Indels 9; Gaps 6;
QY 13 TGAAGCTTGGCGGAGCTTAAACATGCAAGTGAAGGCTTAACAGGAGCTTGCTCC 72
Db 1 TGAAGCTTGGCGGAGCTTAAACATGCAAGTGAAGGCTTAACAGGAGCTTGCTCC 58
QY 73 TGTGACGAGCGGCGGAGCTGAGTAAACGCTAGAGATCTGCTAGTAGAGGGGACAA 132
Db 59 TGAATTC-AGCGGGCGGAGCGGTGAGTAAATGCTAGAGATCTGCTAGTAGAGGGGACAA 117
QY 133 CATGTGAAACGCAATGCTAATACCGCATACCGCTTGAAGGGGAAAGAGGAGACTCTTCG 132
Db 118 CGCTTCGAAAGGAGCGCTAATACCGCATACCGCTTGAAGGGGAAAGAGGAGACTCTTC 175
QY 193 GAGCCTTCGCTATTAGATGAGCTGCGTGAAGATTAGTAGTTGGTGAAGGCTTA 252
Db 176 GGGCCTTGGCTATGAGATGAGCTTGAAGCTTGAAGCTTGGTGAAGGCTTA 235
QY 253 CCAAGGCGAGATCTCTAACTGGTCTGAAGAGATCAAGTCACTGGGAGCTGAGACAC 312

Db 236 CCAAGGCGAGATCTCTAACTGGTCTGAAGAGATGATCACTGACACTGAGATCGAAGAC 295
QY 313 GAGCCAGACTCTTAACGGGAGGACAGCACTAGTGGGAAATTTGACAAATGGGCGCAAGCTGAT 372
Db 296 GGTCCAGACTCTTAACGGGAGGACAGCACTAGTGGGAAATTTGACAAATGGGCGCAAGCTGAT 355
QY 373 CCAGCCATGCCGCTGTGTGAAGAGGCTTAAAGGTTGTAAAGCACTTTCAGGGGTGAG 432
Db 356 CCAAGCAGTCCGCGCTGTGTGAAGAGGCTTTCAGGATTTGTAACCACTTAAAGTGGAGG 415
QY 433 AAGGCTGATAGTTAATACCTTATCATCTTGACGTTAGCCCAAGAAAGACCGGCTTA 492
Db 416 AAGGCACTTAACCTTAATACCTTATGAGTTTGAAGTTAACCAAGAAATTAAGCACCGGCTTA 475
QY 493 CTCGTGCGACAGCCCGGTAATACAGAGGGTGAAGGCTTAATGGAATTAAGCTGAGGCG 552
Db 476 CTCGTGCGACAGCCCGGTAATACAGAGGGTGAAGGCTTAAATGCAATTAATCTGAGCG 535
QY 553 TAAAGCGCGCTAGAGTGGTTTGTAAAGTGGATGTGAATCCAGGGCTCAACCTTGAA 612
Db 536 TAAAGCGCGCTAGAGTGGTTTGTAAAGTGGATGTGAATCCAGGGCTCAACCTTGAA 595
QY 613 TGGCACCCGATCTGCTAGCTAGATGATGTAAGGGGTGTGGAATTTCTGTGTAGCG 672
Db 596 CTGCAATTCAAACTGCAAGCTAGATGATGTAAGGGGTGTGGAATTTCTGTGTAGCG 655
QY 673 GTGAATTCGTAGATATAGAGAGGACATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 732
Db 656 GTGAATTCGTAGATATAGAGAGGACATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 715
QY 733 TGAACCTAGAGTGGGAAAGCGTGGGAGCAAAACGATTAATGATACCTGTAGTCCAGCG 792
Db 716 TGACACTAGAGTGGGAAAGCGTGGGAGCAAAACGATTAATGATACCTGTAGTCCAGCG 775
QY 793 CGTAAGAGTGTACTAGACCGTTGG--GTTGTAAAGACTAGTAGGGCGAGCTAAGCA 850
Db 776 CGTAAGAGTGTACTAGACCGTTGG--GTTGTAAAGACTAGTAGGGCGAGCTAAGCA 835
QY 851 TAAAGTAAACCGCTGGGAGAGTACCGCGCAAGGTTAAACTCAATGATTAAGCGGGCG 910
Db 836 TAAAGTAAACCGCTGGGAGAGTACCGCGCAAGGTTAAACTCAATGATTAAGCGGGCG 895
QY 911 CCGCAAGAGCGGTGAGACATGCTGTTAATTCGAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 970
Db 896 CCGCAAGAGCGGTGAGACATGCTGTTAATTCGAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 955
QY 971 TTGAATTCAGAGAACTTTGAGAGATCAGATGCTGCTTGGGAACTGTGAGACAGGTG 1030
Db 956 TTGAATTCAGAGAACTTTGAGAGATCAGATGCTGCTTGGGAACTGTGAGACAGGTG 1015
QY 1031 CTGCAATGCTGTCTGACAGCTGCTGTGTGAATGTTGGTTAAGTCCCGTAAGAGCGCA 1090
Db 1016 CTGCAATGCTGTCTGACAGCTGCTGTGTGAATGTTGGTTAAGTCCCGTAAGAGCGCA 1075
QY 1091 ACCCTTGCTCTTATTTGACAGACGTAATGATGAGGAACTTAAAGAGACTGCGGTGACA 1150
Db 1076 ACCCTTGCTCTTATTTGACAGACGTAATGATGAGGAACTTAAAGAGACTGCGGTGACA 1135
QY 1151 AACCGGAAAGGTGGGAGCAGCTCAATGATCATGAGCCCTTAAAGAGAGGCTTACAC 1210
Db 1136 AACCGGAAAGGTGGGAGTGAAGCTCAATGATCATGAGCCCTTAAAGAGAGGCTTACAC 1195
QY 1211 CGTGTCAATGAGGCTTATACAGAGAGGCTGCAAGCTAGAGGATGAGAGCGAATCCCAAA 1270
Db 1196 CGTGTCAATGAGGCTTATACAGAGAGGCTGCAAGCTAGAGGATGAGAGCGAATCCCAAA 1255
QY 1271 GTAGCTGTAGTCCGATTTGAGATCTGCAACTGCACTCATGAGATGCGAATGCTTAGTA 1330
Db 1256 ACCGATGTAGTCCGATTTGAGATCTGCAACTGCACTCATGAGATGCGAATGCTTAGTA 1315
QY 1331 ATCGATATGAGATGCTCAAGTGAATAGCTTCCCGGCGCTTATACACACCGCGGCTAC 1390

Db 1316 ATCGGAATCAGAAATGTGCGCGTGAATACGTTCCCGGCGCTTGACACACCGCCGCTCAC 1375
Qy 1391 ACCATGGAGATTGATTGCTCCAGAAAGTACGTTAACTTCGGGAGATGGCGTTACC 1450
Db 1376 ACCAAGGAGAGTGGTTCACCAAGAGTACGTTACCTC- TTCCGAGAGACGTTACC 1433
Qy 1451 ACGAGTGTCAATAGTACTGCGGTTGAAGTCTAC 1483
Db 1434 ACGTGTATTCATGACTGCGGTTGAAGTCTAC 1466

RESULT 7
AAL39554

ID AAL39554 standard; DNA; 1501 BP.

XX AAL39554;

DT 05-SEP-2002 (first entry)

XX Pseudomonas jessenii Pl61 strain DNA.

XX Polyhydroxyalkanoate; PHA; benzoyl alkanolic acid; device material;

XX water repellent; medical material; Pseudomonas jessenii; Pl61 strain; ds.

XX Pseudomonas jessenii.

XX EPI188782-A2.

XX 20-MAR-2002.

XX 14-SEP-2001; 2001EP-0122101.

XX 14-SEP-2000; 2000JP-0279900.

XX 13-DEC-2000; 2000JP-0378827.

XX 31-MAY-2001; 2001JP-0165238.

XX 31-MAY-2001; 2001JP-0165509.

XX 11-SEP-2001; 2001JP-0275063.

XX (CANO) CANON KK.

XX Honma T, Sugawa E, Yano T, Imamura T, Kennoku T;

XX WPI; 2002-481356/52.

XX New polyhydroxyalkanoate useful as device material, water repellent

XX material, and medical material -

XX Disclosure; Page 57; 75pp; English.

XX The invention relates to a novel method for manufacturing

XX polyhydroxyalkanoate (PHA) comprising preparing a medium containing a

XX substituted benzoyl alkanolic acid, and culturing a microorganism capable

XX of synthesizing the PHA using the substituted benzoyl alkanolic acid in

XX the medium. The method also includes the extraction and recovery of PHA

XX from the bacteria culture. PHA is useful as a device material, water

XX repellent material, and a medical material. This polynucleotide sequence

XX represents the DNA of Pseudomonas jessenii Pl61 strain relating to the

XX invention.

XX NOTE: This polynucleotide sequence is shown in the sequence listing,

XX however it is not further described in the specification.

XX

SQ Sequence 1501 BP; 379 A; 339 C; 475 G; 308 T; 0 other;

Query Match 76.1%; Score 1131; DB 24; Length 1501;

Best Local Similarity 88.2%; Pred. No. 0; Mismatches 165; Indels 9; Gaps 6;

Matches 1299; Conservative 0; Mismatches 165; Indels 9; Gaps 6;

Qy 13 TGAACGCTGGCGCGAGGCTTTAAACATGCAAGTCGAGCGGTAAACAGGCGAGCTTGCTCC 72

Db 1 TGAACGCTGGCGCGAGGCTTTAAACATGCAAGTCGAGCGGTAAACAGGCGAGCTTGCTCC 58

Qy 73 TGCTACGAGCGCGAGGCTTGAGTAAAGCTGAGTAAAGCTGAGTAAAGGAGGAGCA 132

Db 59 TGAATTC-AGCGGAGGAGCGGAGTGAATATGCTAGGAATCTGCTGTAGTGGGAGACAA 117

Qy 133 CATGTGAAACGATGCTAATACCGCATACGCCCTTACAGGGGAGAAAGAGGAGACTTTCG 192

Db 118 CGTTCGAAAGGAGCGTAAATACCGCATACGCCCTTACAGGGGAGAAAGAGGAGACTTTCG 175

Qy 193 GAGCCTTCGCTATTAGATAGCCCTGAGATTAAGTATGAGTATGAGGTTAAAGGCTTA 252

Db 176 GGGCTTGCCCTATCAGATAGAGCTAGTGGCTAGGATTAAGTATGAGGTTAAAGGCTTA 235

Qy 253 CCAAGGCGAGATCTCTACTGCTGAGAGGATGACCACTGAGGATGAGACAC 312

Db 236 CCAAGGCGAGATCTCTACTGCTGAGAGGATGAGCACTGAGGATGAGACAC 295

Qy 313 GAGCCAGACTCTACCGGAGGAGCGAGTGGGAGATTAAGCAATGGGCGAGGCTGAT 372

Db 296 GGTCCAGACTCTACCGGAGGAGCGAGTGGGAGATTAAGCAATGGGCGAGGCTGAT 355

Qy 373 CCAAGCCTGCGCGTGTGAGAGAGGCTTAAGGTTGTAAGCACTTTCAGGAGTGAAG 432

Db 356 CCAAGCCTGCGCGTGTGAGAGAGGCTTTCAGGATTTGTAAGCACTTTCAGGAGTGAAG 415

Qy 433 AAGGATATGATTAATAGTTATCATCTGAGCTTACCCGAGAGAGGAGGAGGAGCTTA 492

Db 416 AAGGATATTAATAGTTATCATCTGAGCTTACCCGAGAGAGGAGGAGGAGGAGCTTA 475

Qy 493 CTCTGTGCGAGAGCGCGGCTTAATACAGAGGAGTGAAGGCTTAATGAGATTAATCTGAGG 552

Db 476 CTCTGTGCGAGAGCGCGGCTTAATACAGAGGAGTGAAGGCTTAATGAGATTAATCTGAGG 535

Qy 553 TAAAGCGCGGTAGTGTGTTTGAATGAGATGATTAATCCAGAGGCTTAATCTGAGG 612

Db 536 TAAAGCGCGGTAGTGTGTTTGAATGAGATGATTAATCCAGAGGCTTAATCTGAGG 595

Qy 613 TGGCAGCCGATCTAGGCTAGCTAGATGATGATGAGAGGAGTGAATTTCTGTGAGCG 672

Db 596 CTGATTCAGAACTGACAGCTAGATGATGATGAGAGGAGTGAATTTCTGTGAGCG 655

Qy 673 GTGAATGCGTATATGAGAGAGAACTAGTGGCGAGGAGGAGGAGGAGGAGGAGGAG 732

Db 656 GTGAATGCGTATATGAGAGAGAACTAGTGGCGAGGAGGAGGAGGAGGAGGAGGAG 715

Qy 733 TGAACATGAGTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 792

Db 716 TGAACATGAGTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 775

Qy 793 CGTAAAGATGCTACTAGCCGTTGG- GTTGAATGAGTATGAGTGGCGAGGTTAAGCAG 850

Db 776 CGTAAAGATGCTACTAGCCGTTGG- GTTGAATGAGTATGAGTGGCGAGGTTAAGCAG 835

Qy 851 TGAATAGACCGGCTGGGAGATAGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 910

Db 836 TGAATAGACCGGCTGGGAGATAGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 895

Qy 911 CCGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 970

Db 896 CCGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 955

Qy 971 TTAGCATCCACAGAACTTTGAGAGATCAGATGAGTGGCTTCCGGAATCTGAGACAGG 1030

Db 956 TTAGCATCCACAGAACTTTGAGAGATCAGATGAGTGGCTTCCGGAATCTGAGACAGG 1015

Qy 1031 CTGATGAGTGGCTTCCGGAATCTGAGAGATCAGATGAGTGGCTTCCGGAATCTGAGAC 1090

Db 1016 CTGATGAGTGGCTTCCGGAATCTGAGAGATCAGATGAGTGGCTTCCGGAATCTGAGAC 1075

Qy 1091 ACCCTTGTCTTATTTGCGAGCACTGATGAGTGGGAGGAGGAGGAGGAGGAGGAGGAG 1150

Db 1076 ACCCTTGTCTTATTTGCGAGCACTGATGAGTGGGAGGAGGAGGAGGAGGAGGAGGAG 1135

Qy 1151 AACCGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1210

Db 1136 AACCGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1195

QY 1091 ACCCTGTCCTTATTGCGACGCTATGTTGGGAAGCTTTAAGGAGACTGCCGTGACA 1150
 Db 1076 ACCCTTGCTTATTGTTACGACGTAATGTTGGGCACTTAAGGAGACTGCCGTGACA 1135
 QY 1151 AACCGAGAGAGTGGGGACGACGTCAGTCATCATGCCCCCTTACGAGTAGGGCTACACA 1210
 Db 1136 AACCGAGAGAGTGGGGATGACGTCAGTCATCATGCCCCCTTACGAGTAGGGCTACACA 1195
 QY 1211 CGTGTACAAATGGCCTATPACAGAGGGCTGCAAGCTAGAGTAGAGCAATCCCAACA 1270
 Db 1196 CGTGTCACATGTTGGTACAGAGGGTGGCCAGCCGAGGTGAGCTAATCCCAACA 1255
 QY 1271 GTACGTCTAGTCCGAGTGTGAGTGTGCACTGCACTGCAAGTGGAGTGGTACGA 1330
 Db 1256 ACCGATCGTATCCGAGTGTGAGTGTGCACTGCACTGCAAGTGGAGTGGTACGA 1315
 QY 1331 ATCGGTAATCAGAAATGTACAGGTGATACGTTCCCGGGCTTGTACACACCCCGTCAC 1390
 Db 1316 ATCGGTAATCAGAAATGTACAGGTGATACGTTCCCGGGCTTGTACACACCCCGTCAC 1375
 QY 1391 ACCATGAGAGTGTGATTTGCTCCAGAAAGTAGTAGCTTAACCCCTGCGGAGTGGGTTACG 1450
 Db 1376 ACCATGAGAGTGTGATTTGCTCCAGAAAGTAGTAGCTTAACCCCTGCGGAGTGGGTTACG 1433
 QY 1451 ACGGAGTGTCAATGACTGGGGGTGGAAGTCTAC 1483
 Db 1434 ACGGTGTGATCATGACTGGGGGTGGAAGTCTAC 1466

RESULT 9
 AA166302
 ID AA166302 standard; DNA; 1501 BP.
 AC AA166302;
 XX
 DT 22-JAN-2002 (first entry)
 XX
 DE Pseudomonas jessenii coding sequence.
 XX
 KW Polyhydroxyalkanoate; 3-hydroxyphenylalkanoic acid; PHA;
 KM medical material; biodegradable polymer; ds.
 XX
 OS Pseudomonas jessenii.
 XX
 PN EP1130043-A2.
 XX
 PD 05-SEP-2001.
 XX
 PF 28-FEB-2001; 2001EP-0104922.
 XX
 PR 29-FEB-2000; 2000JP-0054317.
 PR 29-FEB-2000; 2000JP-0054667.
 XX
 PA (CANO) CANON KK.
 XX
 PI Honma T, Yano T, Kobayashi S, Imamura T, Kermoku T, Kozaki S;
 XX
 DR WPI; 2002-012494/02.
 XX
 PT Novel polyhydroxy alkanates containing 3-hydroxy phenyl alkanolic acid
 PS monomer units for use as biodegradable and functional polymers -
 XX
 XX Disclosure; Page 32-33; 46pp; English.
 CC The present invention relates to polyhydroxy alkanates (PHA) containing
 CC 3-hydroxy phenyl alkanolic acid monomer units. These can be used as
 CC biodegradable, bio-compatible, functional polymers, as device material
 CC and as scit medical material. The present sequence is a coding sequence
 CC from Pseudomonas jessenii.
 XX
 SQ Sequence 1501 BP; 379 A; 339 C; 475 G; 308 T; 0 other;

Query Match 76.1%; Score 1131; DB 24; Length 1501;
 Best Local Similarity 88.2%; Pred. No. 0;
 Matches 1299; Conservative 0; Mismatches 165; Indels 9; Gaps 6;

QY 13 TGAACGCTGGCGGCGAGCTTTAAACATGCACTGACGCGTAAACAGGGAGCTTCTCC 72
 Db 1 TGAACGCTGGCGGCGAGCTTTAAACATGCACTGACGCGG-ATGACGGGAGCTTCTCC 58
 QY 73 TGTGACGAGAGCGGGGACGCGGTGATTAACCGGTAGAGAACTGTGCTGTAGAGGGGACAA 132
 Db 59 TGAATTC-AGCGGCGAGCGGGTGAATAGCTTAGGAATCTGCTGTAGTGGGACAA 117
 QY 133 CATGTGAAAACGATGTCTAATACCGCATAGCCCTAGAGGGGAAAGAGAGGACCTTTGG 192
 Db 118 CGTCTGAAAAGGAGCGCTAATACCGCATAGCTTACGGGAGAAAGACAGGGG--CCTTC 175
 QY 193 GAGCTTCCGCTATTAGATAGCCCTGCGTGAAGTTAGCTAGTTGGTGAAGGCTTA 252
 Db 176 GGGCTTGGCGTANCAATAGAGCTTAGTCCGATTAGCTAGTTGGTGAAGGCTTA 235
 QY 253 CCAAGCGAGATCTTAATCTGGTCTGAGAGATGACAGTCACTAGGAGTGAAGAC 312
 Db 236 CCAAGCGAGATCTTAATCTGGTCTGAGAGATGATCACTCACTGAACTGAAGAC 295
 QY 313 GAGCCAACTCTTACGCGGAGGCGACAGTGGGGAAATTTGACAAATGGCGCAAGCTTAT 372
 Db 296 GGTCCAACTCTTACGCGGAGGCGACAGTGGGGAAATTTGACAAATGGCGCAAGCTTAT 355
 QY 373 CCAGCCATGCGCGGTGTGTGAAGAAGCGCTTGGAGCTTTCAAGGGTGAAG 432
 Db 356 CCAGCCATGCGCGGTGTGTGAAGAAGCTTGGAGCTTTCAAGGGTGAAG 415
 QY 433 AAGGGTATAGTTAATACCTTATCATCTTGAAGTACCCGAGAAAGCAACCGGCTTA 492
 Db 416 AAGGGATTAATACCTTATCATCTTGAAGTACCCGAGAAAGCAACCGGCTTA 475
 QY 493 CTCTGTGCCAGACCGCCGCTTAATACAGAGGGTGAAGGTTATCGAAATTAACGGGCG 552
 Db 476 CTCTGTGCCAGACCGCCGCTTAATACAGAGGGTGAAGGTTATCGAAATTAACGGGCG 535
 QY 553 TAAAGCCGCGGTAGTGTGTTGTTAAGTGTGATGTAAGTATCCAGAGGCTCAACTTGA 612
 Db 536 TAAAGCCGCGGTAGTGTGTTGTTAAGTGTGATGTAAGTATCCAGAGGCTCAACTTGA 595
 QY 613 TGGCACTCCGATCTGCTAGCTAGATAGTAAGTAAGGGGTGTGGAATTTCTGTGTAGCG 672
 Db 596 CTGCATTCAAACTGACAACTAGAGTATGTAAGGGGTGTGGAATTTCTGTGTAGCG 655
 QY 673 GTGAATGCGTAGTATAGGAAGAACATCAGTGGCGAAGCGACACCTGACTAATAC 732
 Db 656 GTGAATGCGTAGTATAGGAAGAACATCAGTGGCGAAGCGACACCTGACTAATAC 715
 QY 733 TGACACTGAGGTGCGAAAGCGTGGGAGCAAAACAGATTAGTATCCTGTGTAGCGC 792
 Db 716 TGACACTGAGGTGCGAAAGCGTGGGAGCAAAACAGATTAGTATCCTGTGTAGCGC 775
 QY 793 CGTAAAGATGTCTAATAGCCGTTGG--GTGTAATGATTTAGTGGCGAGCTTAACGCA 850
 Db 776 CGTAAAGATGTCTAATAGCCGTTGGAGCTTTAGCTTTAGTGGCGAGCTTAACGCA 835
 QY 851 TAAGTAGACCGCTGGGAGGTACGCGCGGAGGTTAACTCAATGAATTGACGGGGGC 910
 Db 836 TAAGTAGACCGCTGGGAGGTACGCGCGGAGGTTAACTCAATGAATTGACGGGGGC 895
 QY 911 CCGGACAGGGGTGAGCATGTGTTAATTGAGAGCAACGGGAAGCACTTACTACTC 970
 Db 896 CCGGACAGGGGTGAGCATGTGTTAATTGAGAGCAACGGGAAGCACTTACTACTC 955
 QY 971 TTGACATCCACAGAACATTTGAGAGATGAGTGTGCTTCCGGAACCTGTGAGACAGGTG 1030
 Db 956 TTGACATCCACATGAATTTCAAGAGTGAATGGGTGCTTCCGGAACCTGTGAGACAGGTG 1015
 QY 1031 CTGCATGCTGTGTGACTGCTGTGTGTAATGTTGGTTAAGTCCCGTAACGAGCGCA 1090

QY 1211 CGTGTACATGCGCTATACAGAGGCTGCAAGCTAGGATAGTACGAAATCCCAACAA 1270
 DB 1196 CGTGTACATGCTGTGATACAGAGGCTGCAAGCGGAGTGGACTATATCCCAAAA 1255
 QY 1271 GTACGTGATGTCGGGATTTGAGTCTGCACTGCACTCAGTAAGTGGAAATGCTAGTA 1330
 DB 1256 ACCGATCGTATCCGGATCGAGCTGTGCACTCGAGCTGCGTAAGTGGAAATGCTAGTA 1315
 QY 1331 ATCGGATACAGAAATGTACAGGTAAATCGTTCCCGGGCTTTGACACACCGCCGTCAC 1390
 DB 1316 ATCGGAAACAGAAATGTACAGGTAAATCGTTCCCGGGCTTTGACACACCGCCGTCAC 1375
 QY 1391 ACCATGAGGATGATTTGCTCCAGAGTAGTACTTAACCTTCGCGGATGCGGTTACC 1450
 DB 1376 ACCATGAGGATGATTTGCTCCAGAGTAGTACTTAACCTTCGCGGATGCGGTTACC 1433
 QY 1451 ACGGAGTGTCAATGACTGGGCTTGAAGTCTAC 1483
 DB 1434 ACGGTGTGATTCATGACTGGGCTTGAAGTCTAC 1466

RESULT 8

AA167771
 ID AA167771 standard; DNA; 1501 BP.

AA167771;

27-FEB-2002 (first entry)

Nucleotide sequence of *P. jessenii* strain P161 16S rRNA.

Polyhydroxy alkanoate; PHA; biodegradable; plastic; polymer; 16S rRNA;

microorganism; soil; ds.

Pseudomonas jessenii.

EP1130042-A2.

05-SEP-2001.

28-FEB-2001; 2001EP-0104925.

29-FEB-2000; 2000JP-0054668.

29-FEB-2000; 2000JP-0054669.

27-SEP-2000; 2000JP-0294634.

(CANO) CANON KK.

Homma T, Sugawa E, Yano T, Kobayashi S, Imamura T, Kenmoku T;

WPI; 2002-035635/05.

Novel polyhydroxy alkanoates containing 3-hydroxybenzoyl alkanolic acid

monomer units for use as biodegradable plastic and functional polymers

Disclosure; Page 32-33; 49pp; English.

The invention provides polyhydroxy alkanoates (PHA) comprising

3-hydroxybenzoyl alkanolic acid monomer units and methods for synthesizing

the novel PHAs. The new PHAs are useful as biodegradable plastics for

production of different kinds of products with melting processes, like

conventional plastics. The polyhydroxy alkanoates are useful as bio-

compatible, functional polymers, such as device materials and soft

medical materials. The present sequence represents the basic nucleotide

sequence of 16S rRNA of *P. jessenii* strain P161, a microorganism isolated

from soil that can produce PHAs.

Sequence 1501 BP; 379 A; 339 C; 475 G; 308 T; 0 other;

Query Match 76.1%; Score 1131; DB 24; Length 1501;

Best Local Similarity 88.2%; Fred. No. 0;

Matches 1299; Conservative 0; Mismatches 165; Indels 9; Gaps 6;

QY 13 TGAAGCTGGCGGCGAGGCTTTAAACATGCAATGCAAGCGGTACAGAGGAGCTTGTCTC 72
 DB 1 TGAAGCTGGCGGCGAGGCTTAAACATGCAATGCAAGCGGTACAGAGGAGCTTGTCTC 58
 QY 73 TGTCTAGCAGCGGCGGAGCGGCTGAGTAAACCGTGAAGATGCTGCTAGTAAAGGAGCA 112
 DB 59 TGAATTC-AGCGGCGAGCGGCTGAGTAAATGCTGCTAGTAAATGCTGCTGAGGAGCA 117
 QY 133 CATGTGAACGCAATGCTAATATCCGATACCGCTGAGGCGGAAAGAGGCGACTCTTCG 192
 DB 118 CATTCTGAAAGGAGCGCTAATATCCGATACCGCTGAGGCGGAAAGAGGCGACTCTTCG 175
 QY 193 GAGCGCTTCCGCTAATGAGTAAAGCTGAGTAAAGCTGAGTAAAGCTGAGTAAAGCTGAG 252
 DB 176 GGGCGCTTCCGCTAATGAGTAAAGCTGAGTAAAGCTGAGTAAAGCTGAGTAAAGCTGAG 235
 QY 253 CCAAGGCGAGATCTTAATCTGCTGAGAGATGACCACTCACTGAGCTGAGACAC 312
 DB 236 CCAAGGCGAGATCTTAATCTGCTGAGAGATGACCACTCACTGAGCTGAGACAC 295
 QY 313 GGGCGGAGCTCTTAATGAGTAAAGCTGAGTAAAGCTGAGTAAAGCTGAGTAAAGCTGAG 372
 DB 296 GGTCCAGACTCTTAATGAGTAAAGCTGAGTAAAGCTGAGTAAAGCTGAGTAAAGCTGAG 355
 QY 373 CCAAGGCGAGATCTTAATCTGCTGAGAGATGACCACTCACTGAGCTGAGACAC 432
 DB 356 CCAAGGCGAGATCTTAATCTGCTGAGAGATGACCACTCACTGAGCTGAGACAC 415
 QY 433 AAGGCTGATGATTAATGCTAATCTGAGTAAAGCTGAGTAAAGCTGAGTAAAGCTGAG 492
 DB 416 AAGGCTGATTAATGCTAATCTGAGTAAAGCTGAGTAAAGCTGAGTAAAGCTGAGTAA 475
 QY 493 CTCTGTGCGAGAGCGGCTGATTAATGAGTAAAGCTGAGTAAAGCTGAGTAAAGCTGAG 552
 DB 476 CTCTGTGCGAGAGCGGCTGATTAATGAGTAAAGCTGAGTAAAGCTGAGTAAAGCTGAG 535
 QY 553 TAAAGCGCGCTGAGTAAAGCTGAGTAAAGCTGAGTAAAGCTGAGTAAAGCTGAGTAA 612
 DB 536 TAAAGCGCGCTGAGTAAAGCTGAGTAAAGCTGAGTAAAGCTGAGTAAAGCTGAGTAA 595
 QY 613 TGGGACCGGATGAGTAAAGCTGAGTAAAGCTGAGTAAAGCTGAGTAAAGCTGAGTAA 672
 DB 596 CTGCACTTAAATCTGAGTAAAGCTGAGTAAAGCTGAGTAAAGCTGAGTAAAGCTGAG 655
 QY 673 GTGAATGCGTAAATGAGTAAAGCTGAGTAAAGCTGAGTAAAGCTGAGTAAAGCTGAG 732
 DB 656 GTGAATGCGTAAATGAGTAAAGCTGAGTAAAGCTGAGTAAAGCTGAGTAAAGCTGAG 715
 QY 733 TGAAGCTGAGTAAAGCTGAGTAAAGCTGAGTAAAGCTGAGTAAAGCTGAGTAAAGCTGAG 792
 DB 716 TGAAGCTGAGTAAAGCTGAGTAAAGCTGAGTAAAGCTGAGTAAAGCTGAGTAAAGCTGAG 775
 QY 793 CTTAAAGCTGAGTAAAGCTGAGTAAAGCTGAGTAAAGCTGAGTAAAGCTGAGTAAAGCTGAG 850
 DB 776 CTTAAAGCTGAGTAAAGCTGAGTAAAGCTGAGTAAAGCTGAGTAAAGCTGAGTAAAGCTGAG 835
 QY 851 TAAAGCTGAGTAAAGCTGAGTAAAGCTGAGTAAAGCTGAGTAAAGCTGAGTAAAGCTGAG 910
 DB 836 TAAAGCTGAGTAAAGCTGAGTAAAGCTGAGTAAAGCTGAGTAAAGCTGAGTAAAGCTGAG 895
 QY 911 CCGGCAAGCGGCTGAGTAAAGCTGAGTAAAGCTGAGTAAAGCTGAGTAAAGCTGAGTAAAGCTGAG 970
 DB 896 CCGGCAAGCGGCTGAGTAAAGCTGAGTAAAGCTGAGTAAAGCTGAGTAAAGCTGAGTAAAGCTGAG 955
 QY 971 TTGACATCAAGAAATTTGAGTAAAGCTGAGTAAAGCTGAGTAAAGCTGAGTAAAGCTGAG 1030
 DB 956 TTGACATCAAGAAATTTGAGTAAAGCTGAGTAAAGCTGAGTAAAGCTGAGTAAAGCTGAG 1015
 QY 1031 CTGCAATGCTGCTGAGTAAAGCTGAGTAAAGCTGAGTAAAGCTGAGTAAAGCTGAGTAAAGCTGAG 1090
 DB 1016 CTGCAATGCTGCTGAGTAAAGCTGAGTAAAGCTGAGTAAAGCTGAGTAAAGCTGAGTAAAGCTGAG 1075

Db	955	CCTTGACATGACAGAACTTTCAGAGATGGATTGGGCTTCGGGAACTCGACACAGG	1015
Qy	1029	TGCTGATAGGCTGTGCTCAAGCTCGTGTGTGAATGTTGAGTTAAAGTCCCGTAAAGAGCG	1088
Db	1016	TGCTGATAGGCTGTGCTCAGCTCGTGTGTGAATGTTGAGTTAAAGTCCCGTAAAGAGCG	1075
Qy	1089	CAACCCCTTCTCTTAATTTTGACAGACAGTAATGAGGAACTTTAAGAGACATCGCCGATGA	1148
Db	1076	CAACCTTCTCTTAATTTTGACAGACAGTAATGAGGAACTTTAAGAGAGATCGCCGATGA	1135
Qy	1149	CAAAACGGAGAAAGTGGGGAGACAGACGTCAAGTCATCATAGGCCCTTACGATAGGCGCTTACA	1208
Db	1136	CAAAACGGAGAAAGTGGGGAGATGACATCAAGTCATCATAGGCCCTTACGCGCTGAGCTTACA	1195
Qy	1209	CACGTGCTACATAGGCGGTATACAGAGGCGCTGAAAGTAGAGATAGAGACGAATCCACA	1268
Db	1196	CAGTGCTACATAGGTGTGCGTACAGAGGCTTCCAAAGCCGGAGTGGAGCTAATCTCACA	1255
Qy	1269	AAGTACGTGTGATGTCGGGATTTGGAAGTCTGCACTCGACTCATGAATGTGGAAATGCTTAG	1328
Db	1256	AAACCGATGTGTGTCGGGATGCGAGTCTGCAACTCGACTCGTGAAGTGTGGAAATGCTTAG	1315
Qy	1329	TAACTGTAATAGAAATGTCAAGGGAATACGTTCCCGGCGCTTGTACACACCGCCGCTC	1388
Db	1316	TAACTGCGAATAGAAATGTCCGGGTGAATACGTTCCCGGCGCTTGTACACACCGCCGCTC	1375
Qy	1389	ACACCATGGGAAGTGAATGCTCCAGAAAGTACTAGCTTAAACCTTCGGGGATGCGGATTA	1448
Db	1376	ACACCATGGGAATGAGGTGTGCACCAAGAAAGTACTAGCTAACC--TTCCGGAGAGACGGTTTA	1453
Qy	1449	CCACGGAGTGTCAATGACTGGGAT	1473
Db	1434	CCACGCTGTGATTCATGACTGGGAT	1458

RESULT 12

ID AAL50856 standard; DNA; 1480 BP.

AC AAL50856;

DT 30-JAN-2003 (First entry)

DE Benzene-degrading bacteria-related DNA sequence #2.

KW Benzene-degrading bacteria; benzene decomposition; ds.

OS. Unidentified.

PN KR2002011252-A.

PD 08-FEB-2002.

PF 01-AUG-2000; 2000KR-0044629.

PR 01-AUG-2000; 2000KR-0044629.

PA (SMSU) SAMSUNG EVERLAND INC.

PI Park JH;

DR WPI; 2002-572306/61.

PT Benzene-degrading bacteria and its utilization method -

PS Disclosure; Fig 1; 7pp; Korean.

CC The invention comprises a strain of bacteria (*Pseudomonas putida*) that is

CC 1500ppm). The present DNA sequence is shown in a figure of the

[illegible]

Query Match 75.5%; Score 1121.4; DB 24; Length 1480;
Best Local Similarity 88.1%; Pred. No. 0;
Matches 129; Conservative 0; Mismatches 166; Indels 9; Gaps 6;

OY	1	ATTGAACGCTGGCGGACAGCTTTAAACACATGCAAGTCGACGGTTAACAGGGGAGCTTGGT	70
Db	1	ATTGAACGCTGGCGGACAGGCTTAAACACATGCAAGTCGACGGTATGCAAGGAGCTTGGT	58
OY	71	CTGTGACGACGCGGCGGACGGGTGAAATACCGGTAGAAATCTGCTTAGTAGAGGGGAC	130
Db	59	-CTTCGATTCACCGGCGGACGGGTGAAATGCTGTAGAAATCTGCTTAGTAGAGGGGAC	117
OY	131	AACATGSGAAGGATGCTATATACCGCATACGCGCTGAGGGGGGGAAGAAGGGGACTCTT	190
Db	118	AACGTTTGGAAAGAACCTTATACCGCATACGCTTACCGGGAAGAAAGACGGGGA-CTT	175
OY	191	CGGAGCCTTCGCTATTAGATGAGCCTCGGTGAAATTAGCTAGTTGGTAGGGTTAAAGCC	250
Db	176	TGGGGCTTCGCTATCAGATGACCTTAGGCGGATTAAGCTAGTTGGTAGGGTTAAAGCC	235
OY	251	TACCAAGGGAAGATCTTACTGTGCTGAGAGATGACACAGTCACACTGGGACACTGAC	310
Db	236	CACCAAGGGAAGATCTGCTGATGCTGAGAGATGATAGTCACACTGGAACCTGAGAC	295
OY	311	ACGAGCCACACTCTTACCGGAGGACGAGAGTGGGGAATTATGCACAATGGGCGCAAGCTTG	370
Db	296	ACGGTCACAGCTCTTACCGGAGGACGAGAGTGGGGAATTATGCACAATGGGCGCAAGCTTG	355
OY	371	ATCCAGCCATGCGCGGTGTGAAAGAGCCTTAGGGTTGTAAGCACTTTAGAGGGTGA	430
Db	356	ATCCAGCCATGCGCGGTGTGAAAGAGCCTTGGATTGTAAGCACTTTAAGTTGGGA	415
OY	431	GGAAGGATATAGTTAATACGTTATATCTTACGTTAGCCCGACAAACACACGGCT	490
Db	416	GGAAGGCACTTAACCTATATCGTTAAGTTTGAACGACAAATPAACACCGGT	475
OY	491	AATCTGTGTCCAGACGCCCGGCTAATACAGAGGTGCAGCCTTATCGGAATTTACTGG	550
Db	476	AATCTGTGTCCAGACGCCCGGCTAATACAGAGGTGCAGCCTTATCGGAATTTACTGG	535
OY	551	CGTAAAGCCGCGTAGGTGTTGTTAAGTCGATGTGAAATCCAGGGCTCAACCTTGG	610
Db	536	CGTAAAGCCGCGTAGGTGTTGTTAAGTTGATGTGAAAGCCCGGGCTCAACCTGG	595
OY	611	AATGGAACCCGATACCTGGCTAGCTAGAGTATGTAAGAGGGGTGGAATTTCTCTGTAG	670
Db	596	AATGGAATCAAAATGGCAAGCTAGAGTACGTAAGAGGGGTGGAATTTCTCTGTAG	655
OY	671	CGGTGAATGCTAGATATGGAAGAACTCAGTGGCGAAGCGACACCTCGACTAT	730
Db	656	CGGTGAATGCTAGATATGGAAGAACTCAGTGGCGAAGCGACACCTCGACTAT	715
OY	731	ACTGACACTGAGAGTCCGAAAGCTGTGGGAGCAAAACAGATTAGATTCCTTGGTACTCAC	790
Db	716	ACTGACACTGAGAGTCCGAAAGCTGTGGGAGCAAAACAGATTAGATTCCTTGGTACTCAC	775
OY	791	GCCGTAAAGATGTACTAGCCGTTGGGTT--GTATGACTTAGTGGCGACTPAAGC	848
Db	776	GCCGTAAAGATGTACTAGCCGTTGGGATCCTTAGATTATAGTGGCGACTPAAGC	835
OY	849	AATAGATGACCGCTGGGGAGTACGGCGCGCAAGTTAAATCTCAATGATATTGACGGGG	908
Db	836	ATTAAATTTACCGCTGGGGAGTACGGCGCGCAAGTTAAATCTCAATGATATTGACGGGG	895
OY	909	GCCCGACAAGCGGTGAGCATGTGTATTATCGAAGCAACGCGAAGAACTTACTTAC	968
Db	896	GCCCGACAAGCGGTGAGCATGTGTATTATCGAAGCAACGCGAAGAACTTACTTAC	955
OY	969	TCTTGAATCCACAGAAATTTGAGAAATCAGATGTCCTTGGGAACTGTGAAACAG	1028
Db	956	CTTGAATCCACAGAAATTTTCCAGAAATGATTTGGCTTTCGGGAATCTTGAACAG	1015

OY	423	AGGGGTAGGAGAGGAGTATAGGTTATACGTTATATACGTTACGTTACCCCAAAAG	482
OY	423	AGGGGTAGGAGAGGAGTATAGGTTATACGTTATATACGTTACGTTACCCCAAAAG	482
Db	436	AGUGGAGAGAGAGGAGGAGUAAUUAUACUUCUGUCUUAUACAAAGAAUAAAG	495
OY	483	CACCGGCTAACTGTGCGACGACCGCGGTATATCAAGAGAGTGCAACGTTAATCGAA	542
Db	496	CACCGGCTAACTGTGCGACGACCGCGGTATATCAAGAGAGTGCAACGTTAATCGAA	542
OY	496	CACCGGCTAACTGTGCGACGACCGCGGTATATCAAGAGAGTGCAACGTTAATCGAA	542
OY	543	TTACTGGAGCTAAGAGGCGGATGAGGTATTATTAAGTCGAGATGGAATCCAGGGCTC	602
Db	556	TTACTGGAGCTAAGAGGCGGATGAGGTATTATTAAGTCGAGATGGAATCCAGGGCTC	602
OY	603	AACTTGGAAATGACACCCGATCTGGCTAGCTAAGTATGTTAGAGGGGTGTGAAATTC	662
Db	616	AACTTGGAAATGACACCCGATCTGGCTAGCTAAGTATGTTAGAGGGGTGTGAAATTC	662
OY	663	CTGTGTAGCGGTGAAAATGCGTATGATTTAGAGAGGAACTCACTGCGCAAGCGCACCTT	722
Db	676	CTGTGTAGCGGTGAAAATGCGTATGATTTAGAGAGGAACTCACTGCGCAAGCGCACCTT	722
OY	723	GGACTAATACTGACACTGAGTGTGCGAAACGTGGGAGCAAAACAGATTAGATCCCTGG	782
Db	736	GGACTAATACTGACACTGAGTGTGCGAAACGTGGGAGCAAAACAGATTAGATCCCTGG	782
OY	783	TAGTCCACGCGCGTAAACGATGTCTATAGCCGTTGGGTT--GTATAGCTTAGTGGGCA	840
Db	796	TAGTCCACGCGCGTAAACGATGTCTATAGCCGTTGGGTT--GTATAGCTTAGTGGGCA	840
OY	841	GCTAACGCAATATAGTAAACCGCTGGGAGTACGCGCGCAAGTTAAAACTCAATAGAT	900
Db	856	GCTAACGCAATATAGTAAACCGCTGGGAGTACGCGCGCAAGTTAAAACTCAATAGAT	900
OY	901	TGACGGGGGGCGCCCAAGCGGGAGAGCATGTGTTTATGAAAGCAAGCGAAAGACC	960
Db	916	TGACGGGGGGCGCCCAAGCGGGAGAGCATGTGTTTATGAAAGCAAGCGAAAGACC	960
OY	961	TTACTCTACTTGTGACATCCACAGAACTTTGAGATCAGATGTTGCTTGGGAACTGT	1020
Db	976	TTACTCTACTTGTGACATCCACAGAACTTTGAGATCAGATGTTGCTTGGGAACTGT	1020
OY	1021	GAGACAGATCTCTGATCAGTGTGTGATGCTGTGTGTGAAATGTTGGTTAATGCTCCG	108
Db	1036	GAGACAGATCTCTGATCAGTGTGTGATGCTGTGTGTGAAATGTTGGTTAATGCTCCG	108
OY	1081	AACGAGCGCAACCTTGTCTTATTTGGCAGCAGTAAATGTTGGGAACTTTAAGAGACT	114
Db	1096	AACGAGCGCAACCTTGTCTTATTTGGCAGCAGTAAATGTTGGGAACTTTAAGAGACT	114
OY	1141	GCGGATGACAAACCGAGAGAGAGTGGGAGCAGCATGATCATGAGCCCTTACAGAT	120
Db	1155	GCGGATGACAAACCGAGAGAGAGTGGGAGCAGCATGATCATGAGCCCTTACAGAT	120
OY	1201	GGGCTACACAGCTGTCTTAAATGACGATACAGAGGCTGCAAGCTTACGATAGTAGCGCA	126
Db	1215	GGGCTACACAGCTGTCTTAAATGACGATACAGAGGCTGCAAGCTTACGATAGTAGCGCA	126
OY	1261	ATCCCAACAAGTACGTCGTATGTCGAGATTGGAGTGTGAACTGCACTCAAGTAAGTCGA	132
Db	1275	ATCCCAACAAGTACGTCGTATGTCGAGATTGGAGTGTGAACTGCACTCAAGTAAGTCGA	132
OY	1321	ATGCGTATGATATGCTGAATCAGAAATGTCAAGGTGATACGTTCCCGGACCTTGTACAC	138
Db	1335	ATGCGTATGATATGCTGAATCAGAAATGTCAAGGTGATACGTTCCCGGACCTTGTACAC	138
OY	1381	CGCCGCTACACCATGGAGTGTGATGCTCCAGAAATGATGATTAACCTTCGAGGAT	144
Db	1395	CGCCGCTACACCATGGAGTGTGATGCTCCAGAAATGATGATTAACCTTCGAGGAT	144
OY	1441	GGCGGTTACACGGAATGTGCTAATGACTGTGGGTTGAAATCTA	1482
Db	1453	GGCGGTTACACGGAATGTGCTAATGACTGTGGGTTGAAATCTA	1482

RESULT 15	
AS11023	
ID	AS11023 standard; DNA; 1467 BP.
XX	
XX	
AC	AS11023;
XX	
DT	24-OCT-2001 (first entry)
XX	
DE	Pseudomonas aeruginosa 16s ribosomal RNA gene.
XX	
KW	Antisense; bacterial 16s ribosomal RNA; rRNA; bacterial infection;
KW	human; food grain supplement; livestock; poultry; therapeutic; ds.
XX	
OS	Pseudomonas aeruginosa.
XX	
FN	WO200142457-A2.
XX	
PD	14-JUN-2001.
XX	
PF	29-NOV-2000; 2000WO-US42391.
XX	
PR	29-NOV-1999; 99US-0168150.
XX	
PA	(AUIB-) AVI BIOPHARMA INC.
XX	
PI	Iversen PL;
XX	
DR	WPI; 2001-457295/49.
XX	
XX	Antibacterial compound, useful for treating bacterial infections and as
PT	livestock and poultry food supplement, comprises antisense
PT	oligonucleotides complementary to bacterial 16S and 23S rRNA -
PS	
PS	Disclosure; Page - ; 62pp; English.
XX	
CC	AS11021-AS11034 represent the coding sequences of bacterial 16S
CC	ribosomal RNA (rRNA) genes. The sequences were used to design anti-
CC	bacterial compounds comprising substantially unchanged antisense
CC	oligonucleotides containing 8-40 nucleotide subunits, including a targeting
CC	nucleic acid sequence at least 10 nucleotides in length which is
CC	complementary to a bacterial 16S or 23S rRNA nucleic acid sequence.
CC	The antisense oligomers are used for treating a bacterial infection
CC	in a human or a mammalian animal produced by Escherichia coli, Salmonella
CC	typhimurium, Pseudomonas aeruginosa, Vibrio cholerae, Neisseria
CC	gonorrhoeae, Helicobacter pylori, Bartonella henselae, Haemophilus
CC	influenzae, Shigella dysenteriae, Staphylococcus aureus, Mycobacterium
CC	tuberculosis, Streptococcus pneumoniae, Treponema pallidum and Chlamydia
CC	trachomatis. The antibacterial compound may be used as a food grain
CC	supplement in livestock and poultry food composition.
CC	Note: The present sequence is not shown in the specification but has
CC	been accessed from Genbank using the appropriate accession number given
CC	in the specification.
XX	
XX	
Sequence	1467 BP; 370 A; 330 C; 458 G; 309 T; 0 other;
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Query Match	74.0%; Score 1100.2; DB 22; Length 1467;
Best Local Similarity	88.2%; Pred. No. 0;
Matches 1231; Conservative	0; Mismatches 158; Indels 6; Gaps 3;
QY	81 AGCGGCGACGGGTGAGTAAAGCGCTAGAAATCTGCTTAGTAGAGGGGCAACATGTGGA 140
DB	26 AGGGGGGACGGGTGAGTAAAGCGCTAGAAATCTGCTTAGTAGAGGGGCAACATGTGGA 85
QY	141 AACGATGCTAATACCGATACGCCCTAGAGGGGAAAGAGGGGACTCTTGGAGACTTC 200
DB	86 AAGGAACGCTAATACCGATACGCCCTAGAGGGGAAAGAGGGGGA--CCTTCGGGCTTGG 143
QY	201 CGCTTAGTAGAGGAGCGCTGCGTAGATTAGCTAATTTGGTAGGCTTAAAGGCTTACAAAGCG 260
DB	144 CGCTTAGTAGAGGAGCGCTAAGTTCGATTAGCTAATTTGGTAGGCTTAAAGGCTTACAAAGCG 203
QY	261 AGGATCTCTAACTGGTCTGAGAGGATGACCAGTTCACACTGGGACTGAGACACGCGCCACGA 320

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 30, 2004, 18:26:40 : Search time 3491.17 Seconds

(without alignments)
10345.086 Million cell updates/sec

Title: US-09-737-297-1

Perfect score: 1486

Sequence: 1 gtagctcagatcgacgct.....ctggggctgagcttcacgcg 1486

Scoring table: IDENTITY_NUC

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
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2: em_esthum:*
3: em_estin:*
4: em_estma:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_estc:*
9: gb_est1:*
10: gb_est2:*
11: gb_est3:*
12: gb_est4:*
13: gb_est5:*
14: gb_est6:*
15: em_estum:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vit:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rtd:*
26: em_gss_phg:*
27: em_gss_vit:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	598.6	40.3	1010	29	BZ431523

5	594	40.0	1079	28	BH705272	BH705272
6	591.4	39.8	1044	29	BZ463550	BZ463550
7	591.4	39.8	1051	29	BZ494182	BZ494182
8	590.4	39.7	1016	29	BZ426201	BZ426201
9	589.8	39.7	1031	28	BH656222	BH656222
10	588.6	39.6	741	14	CD042372	CD042372
11	587.8	39.6	1077	29	BZ450751	BZ450751
12	576	38.8	899	29	BZ685785	BZ685785
13	571.6	38.5	1054	28	BH647750	BH647750
14	566.2	38.1	974	29	BZ440868	BZ440868
15	567.2	37.5	1069	29	BZ474941	BZ474941
16	553.8	37.3	699	14	CD043647	CD043647
17	552.6	37.2	1106	29	BZ459292	BZ459292
18	550.8	37.1	951	28	BH651765	BH651765
19	549.4	37.0	641	14	CD040169	CD040169
20	548.2	36.9	1068	29	BZ576668	BZ576668
21	542	36.5	901	29	BZ461852	BZ461852
22	539.8	36.3	674	14	CD044496	CD044496
23	538.4	36.2	977	29	BZ459292	BZ459292
24	535.6	36.0	918	29	BZ437960	BZ437960
25	531.4	35.8	947	29	BZ464837	BZ464837
26	528	35.5	1143	28	BH814866	BH814866
27	526.2	35.4	995	28	BH700021	BH700021
28	524.8	35.3	905	29	BZ572385	BZ572385
29	524.2	35.3	1033	29	BZ561605	BZ561605
30	523.2	35.2	1020	29	BH685417	BH685417
31	517.4	34.8	660	9	AW600903	AW600903
32	513.2	34.5	873	28	BH705306	BH705306
33	512.6	34.5	889	29	BZ426275	BZ426275
34	511.6	34.4	842	28	BH486252	BH486252
35	511.4	34.4	837	29	BZ483676	BZ483676
36	510.8	34.4	862	28	BH527452	BH527452
37	508.8	34.2	846	28	BH562180	BH562180
38	507.8	34.2	835	28	BH552149	BH552149
39	507.6	34.2	1036	29	BZ502068	BZ502068
40	506.8	34.1	604	10	BE204135	BE204135
41	504.8	34.0	848	28	BH730827	BH730827
42	504.8	34.0	857	28	BH578853	BH578853
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ALIGNMENTS

RESULT 1
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DEFINITION LMGtag746 MG1363 Random Sequence Tag Library Lactococcus lactis
SUBSP. cremoris genomic, genomic survey sequence.

ACCESSION BH771024
VERSION BH771024.1 GI:20373981
KEYWORDS GSS.

SOURCE Lactococcus lactis subsp. cremoris
ORGANISM Lactococcus lactis subsp. cremoris
Bacteria: Firmicutes; Lactobacillales; Streptococcaceae;

REFERENCE 1 (bases 1 to 6499)
AUTHORS Bolotin, A., Ehrlich, S.D. and Sorokin, A.
TITLE Studies of genomes of dairy bacteria Lactococcus lactis
JOURNAL Sci. Aliments, (2002) In press
COMMENT Contact: Sorokin A
Genetique Microbienne

INRA, Domaine de Vilvert, 78352 Jouy en Josas cedex, France
Tel: 33 1 34 65 25 16
Fax: 33 1 34 65 25 21
Email: sorokine@jouy.inra.fr
best homologue in strain IL1403 is ywGA (78%)
Class: Sholiquin
High quality sequence start: 30
High quality sequence stop: 6471.

FEATURES

Source

Location/Qualifiers
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Query Match 54.9%; Score 815.2; DB 28; Length 6499;
 Best Local Similarity 76.4%; Pred. No. 1e-229;
 Matches 1132; Conservative 0; Mismatches 333; Indels 17; Gaps 10;

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 544 TGGCTCAGAGCGAACCTGCGCGCTGCT-ATTACATGCAAGTTGACGATGAAGATTG 602
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 603 GTGCTTGCACAATTGGAAGAGCAGCAAGCGGTGAGTAAAGCGGGAATCTGCTTT 662
 120 TAGAGGGGACCAATGTGGAACGCGATGCTAATACCGCATACGCGCTGAGGGGGAAG- 178
 663 GAGCGGGGACCAATTTGGAACGAACTGTAATACCGCATTAATTAACCTTAAACATTAAGT 722
 179 ----GAGGGGACTCTTGGAGCCTTCGCTATTAAATGAGCCTGCTGAGATTAGTACT 234
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 783 TGGTAGGTTAAAGGCTTCCAAAGGCGATGATACATACCGCATTAATTAACCTTAAACATTAAGT 842
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QY 832 AGTGGCGACGCTAAGCAATTAAGTAGACCCGCTTGGGAGTAGACGCCGCAAGTTAAACT 891
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 QY 892 CAATGAATTAAGCGGGGCGCGCAAGCGGTGAGCATGTGTTTAAATGGAAGCAAG 951
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 DB 1562 GGAACCTGAGACAGGTGCTGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1621
 QY 1622 AAGTCCCGAAGAGCGCAACCTTATGTTAGTTCATCA--TTAAGTTGGGCACTCT 1679
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 QY 1680 AAGGAGCTGCGCGTGAACAAACCGAGAGAGTGGGAGAGACATCATATGAGCC 1739
 DB 1192 TTACAGTAGGAGCTACACAGTGTACATGCGTATACAGAGGCTGCAAGCTAGCAT 1251
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 DB 1252 AGTGAAGCAATCCCAAGATGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1311
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 DB 1312 GAAGTGTGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1371
 QY 1860 GAAGTGTGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1919
 DB 1372 TGTACACCGCGCTCAACCATGAGGATGATGATGATGATGATGATGATGATGAT 1431
 QY 1920 TGTACACCGCGCTCAACCATGAGGATGATGATGATGATGATGATGATGATGAT 1473
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 QY 1979 -GCAAGAGAGGCGCTTCTTAAGTAAAGCCATGATGAGGAT 2019
 DB

RESULT 2
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 DEFINITION genomic survey sequence.
 ACCESSION B2439740
 VERSION B2439740.1 GI:26695676
 KEYWORDS GSS.
 SOURCE Brassica oleracea
 ORGANISM Brassica oleracea
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 ; eurosids II; Brassicales; Brassicaceae; Brassica.
 REFERENCE 1 (bases 1 to 1084)
 AUTHORS Town,C.D., Van Aken,S., Uteback,T., Koo,H. and Frazer,C.M.
 TITLE Whole genome shotgun sequencing of Brassica oleracea
 JOURNAL Unpublished
 COMMENT Other GSSs: BONDUS4TR
 CONTACT: Chris Town

TIGR
 712 Medical Center Drive, Rockville, MD 20850, USA.
 Tel: 301-838-3523
 Fax: 301-838-0208
 Email: cdtown@tigr.org
 DNA is from a doubled haploid provided by Tom Osborn.
 Seq primer: TF
 Class: sheared ends.
 Location/Qualifiers

FEATURES

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total DNA inserted into pHD51 using BstXI linkers"
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Best Local Similarity 75.8%; Pred. No. 5.5e-171;
Matches 825; Conservative 0; Mismatches 234; Indels 29; Gaps 4;

QY 250 CTACCAAGGCGACATCTTCTACTGCTGCTGAGAGATGACCACTGAGGACTGAGA 309
DB 3 CTTACAGGCGATATCATGATGCTGCTCCAGAGAGA-GATCAGCCCACTGGGACTGAGA 61
QY 310 CACGCGCCAGACTCTCTACGGGAGGACAGTGGGAAATATTGAGCAATGGGCGCAAGCCT 369
DB 62 CACGCGCCAGACTCTCTACGGGAGGACAGTGGGAAATTTTCCGCAATGGGCGAAAGCCT 121
QY 370 GATCCAGCATGCCGCGTGTGTGAAGAGCCCTTAGCGTTGAAGCACTTTCAGGGGTG 429
DB 122 GACGAGCAATGCGCGCTGAGGTGAAGAGCCCTAGCGGTCTGAACTTCTTTTCCAGAG 181
QY 430 AGGAAGGGTGATAGGTATATCATCTTACCTTACCTTACGCCCCAGAGAGACCCGCG 489
DB 182 AAGAAAG-----CAATGACGATATCTGGGAAATTAAGCATCGCG 218
QY 490 TAACTCTGTGCGACAGCCCGGTATATACAGAGGGTGAAGCCTTATCGAATTAATCTG 549
DB 219 TAACTCTGTGCGACAGCCCGGTATATACAGAGAGTGAAGCAAGCTTATCGAATTAATCTG 278
QY 550 GCGTAAAGCGCGCTAGTGTGTTGTTAAGTCGAGTGAATCCAGAGGCTCAACCTTG 609
DB 279 GCGTAAAGCGCTAGTGTGTTGTTAAGTCGAGTGAATCCAGAGGCTCAACCTTG 338
QY 610 GAATGGAACCCGATCTGCTAGTGTAGATGATGATGAGGGGTGTGGAATTTCCGTGTA 669
DB 339 GACAGCGGTGGGAACCTTACCAAGTGTAGATGATGATGAGGGGTGTGGAATTTCCGTGTA 398
QY 670 GCGGTGAATGCGTATATAGAGAGACATAGTGGCGAAGCGCACCTCTGACTTAA 729
DB 399 GCGGTGAATGCGTATATAGAGAGACATAGTGGCGAAGCGCACCTCTCTGCGACGGA 458
QY 730 TACTGACACTGAGGTGCGAAGCGTGGGAGCAAAAGGATTAGATACCTCTGTAGTCCA 789
DB 459 CACTGACACTGAGAGAGAAAGCTTAGGGAGCGAATGGGATTAGATACCTCTGTAGTCTCT 518
QY 790 CGCGGTAAAGCATGTCTACTAGCCGTTG---GGTGTGAATGACTTATAGTGGCGACCTAAC 846
DB 519 AGCGGTAAAGCATGTACTAGGCGGTGCTGCTGATGCAACCGGTGACGTCTGTACTAAC 578
QY 847 GCATATAGTGAACCGCTGGGAGTATAGGCGCGCAAGGTTAACTCAATGATTAATGACGG 906
DB 579 GCGTTAAGTATCCGCTGGGAGTATAGTGGCGCAAACTCAATGATTAATGACGG 638
QY 907 GGGCGCGCACAGGCGTGGAGAGATGTTGTTAATTCGAAAGCAACGCGAAGAACTTACT 966
DB 639 GGGCGCGCACAGGCGTGGAGAGATGTTGTTAATTCGAAAGCAACGCGAAGAACTTACT 698
QY 967 ACTTTGACATCCACAGAAATTTGAGAGATCAGATGCTGCTCGGGAAGCTGTAGACA 1026
DB 699 GGGCTTACATGCGCGCAATCTCTTGAAGAGAGAGGGTGCCTTCGGGAACCGGACACA 758
QY 1027 GGTCTGCAATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1086
DB 759 GGTCTGCAATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 818
QY 1087 CGCAACCTTGTCTTATTGCGACAGCATATGTTGGGGAATTTAAGAGACTGCGCGT 1146

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DB 819 CGCAACCTTGTCTTATTGCGCA--CGTTGAGTTTGAACCTTGAACGACTGCGCT 876
QY 1147 GACAAACCGGAGAGAGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1206
DB 877 GATTAAGCGGAGAGAGAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 936
QY 1207 CACACGCTTACATAGGCGGTATACAGAGGCTGCAAGCTAGAGATGAGAGAGAGAG 1266
DB 937 CACACGCTTACATAGGCGGTATACAGAGGCTGCAAGCTAGAGATGAGAGAGAGAG 996
QY 1267 CAAAGTACGCTAGTCCGATGAGTGTGCACTGCACTGCACTGCACTGCACTGCACT 1326
DB 997 AAAACCGGTCTCCATGCTGATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1056
QY 1327 AGTAATCG 1334
DB 1057 AGTAATCG 1064

RESULT 3
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LOCUS BZ447500
DEFINITION BONKRF40TR BO.1.6.2_KB tot Brassica oleracea genomic clone BONKRF40,
ACCESSION BZ447500
VERSION BZ447500.1 GI:26712943
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE Town,C.D., Van Aken,S., Uteirack,T., Koo,H. and Fraser,C.M.
TITLE Whole genome shotgun sequencing of Brassica oleracea
JOURNAL Unpublished
COMMENT Other GSSs: BONKRF40TF
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq Primer: TR
Class: sheared ends.
FEATURES
source
1..1053
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="TO100DH3"
/db_xref="taxon:3712"
/clone="BONKRF40"
/clone_1kb="BO.1.6.2_KB tot"
/notes="vector: pHD51, Site 1: BstXI, 1.6-2 kb sheared
total DNA inserted into pHD51 using BstXI linkers"
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Query Match      40.7%; Score 605; DB 29; Length 1053;
Best Local Similarity 75.5%; Pred. No. 7.5e-168;
Matches 815; Conservative 0; Mismatches 235; Indels 29; Gaps 4;

QY 212 GAGCTGCGTGAATTAAGTATGTTGTTAGGTTAAAGGCTTACCAAGGCGAGATCTCTA 271
DB 1053 GGGCTGCGTCTGATTAAGTATGTTGTTAGGTTAAAGGCTTACCAAGGCGAGATCTCTA 994
QY 272 CTGCTGAGAGAGATGACAGTCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 331
DB 993 CTGCTGAGAGAGATGATAGCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 934
QY 332 GGCAGAGATGGGGAAATTTGAGCAATGGGCGCAAGCTGATTCAGAGCATGCCGCTGTGT 391

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Db 933 GGGAGCAGTGGGAA-TTCCGCAATGGGCGAAACCTGACGACCATGCGGCTGAG 875
 Qy 392 GAAGAAGCCTTGGGCTTGAAGCACTTCAGGGGTGAGAGAGGATGATAGTTATAC 451
 Db 874 GTGAAGGCTTACGGGCTCTGAATCTTTTCCAGAGAGAG----- 831
 Qy 452 GTTATCATCTTGAAGTGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 511
 Db 830 -----CATGACGCTATCTGGGAGATTAAGCATGAGCTAACTGTGCGACGCGG 778
 Qy 512 GTAATCAGAGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 571
 Db 777 GTATATCAG 718
 Qy 572 TTGTATAGTGGATGTAATCCAGAGGCTCAACCTTGAATGAGAGAGAGAGAG 631
 Db 717 TTTTAAATCCCGCTCAATCCAGAGGCTCAACCTTGAATGAGAGAGAGAGAG 658
 Qy 632 GCTAGAGATGTAAGAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 691
 Db 657 GCTTGAAGTGGAG 598
 Qy 692 GAAGAAGCATCAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 751
 Db 597 GAAGAAGCATCAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 538
 Qy 752 CGTGGAG 811
 Db 537 CTAG 478
 Qy 812 CCGTGGAGT---TGTATAGTATAGTGGAGAGAGAGAGAGAGAGAGAGAGAG 868
 Db 477 GCGCTGGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 418
 Qy 869 AGTACGCGGAG 928
 Db 417 AGTACGCGGAG 358
 Qy 929 ATGTGATTAATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 988
 Db 357 ATGTGATTAATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 298
 Qy 989 TTGAGAGATCAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1048
 Db 297 TCTTGAAG 238
 Qy 1049 CTGTGTTGGAATTTGGGTTAAGTCCCGTAAAGAGAGAGAGAGAGAGAGAGAG 1108
 Db 237 CTGTGCGGAG 178
 Qy 1109 CAGCAGATATGAG 1168
 Db 177 CA---CGGTGAGTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
 Qy 1169 ACAGAGTGAATGATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1228
 Db 119 ATACAGTGAATGATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60
 Qy 1229 ACAGAGGCTGAG 1287
 Db 59 ACAAGGCTGAG 1

RESULT 4
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 LOCUS BONHD88Tf BO.1.6.2_KB_for Brassica oleracea genomic clone BONHD88,
 DEFINITION genomic survey sequence.
 ACCESSION BZ431523
 VERSION BZ431523.1 GI:26677309
 KEYWORDS GSS.
 SOURCE Brassica oleracea

ORGANISM Brassica oleracea
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 ; eurosids II; Brassicales; Brassicaceae; Brassica.
 REFERENCE 1 (bases 1 to 1010)
 AUTHORS Tom, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M.
 TITLE Whole genome shotgun sequencing of Brassica oleracea
 JOURNAL Unpublished
 COMMENT Other GSSs: BONHD88Tf
 CONTACT: Chris Town
 TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA.
 Tel: 301-838-3523
 Fax: 301-838-0208
 Email: cdtown@tigr.org
 DNA is from a doubled haploid provided by Tom Osborn.
 Seq primer: TP
 Class: sheared ends.
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 source location/Qualifiers
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 /mol_type="genomic DNA"
 /strain="TO100DH3"
 /db_xref="taxon:3712"
 /clone="BONHD88"
 /clone_lib="BO.1.6.2_KB_for"
 /note="Vector: pHD31, Site 1: BstXI, 1.6-2 kb sheared
 total DNA inserted into pHD31 using BstXI linkers"
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 Best local similarity 76.1%; Pred. No. 5.8e-166;
 Matches 788; Conservative 0; Mismatches 219; Indels 28; Gaps 3;
 Qy 224 GATTAGCTAGTTGGTGAAGGATTAAGGCTTACCAAGGAGCATCTTACTGTCTGAGAG 283
 Db 1010 GATTAGCTAGTTGGTGAAGGATTAAGGCTTACCAAGGAGCATATGATGCTGCTCGAGAG 951
 Qy 284 GATGACAGTACACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 343
 Db 950 GATGATCAGACACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 891
 Qy 344 GATATTTGACATGAG 403
 Db 890 GATATTTGCGCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 831
 Qy 404 AGGTTTGAAGCACTTTCAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 463
 Db 830 CCGTCTGCACTTCTTTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 794
 Qy 464 AGCTAGAGCCGAG 523
 Db 793 AGCGATCTGGGAG 724
 Qy 524 GTGCAAGCTTAATGGAATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 583
 Db 733 ATGCAAGGCTTAATGCGATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 674
 Qy 584 ATGTGAATTCAG 643
 Db 673 CCGTCAATTCAG 614
 Qy 644 TAGAGGAGTGAATTTCTGTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 703
 Db 613 TAGGGGCAAGAGAGATTTCCGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 554
 Qy 704 GTGGGAG 763
 Db 553 AGCGGAG 494
 Qy 764 ACAGAGTTAGATACCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 820

Db 493 ATGGATTAGATACCCCGTAGTCTTACCCCTAAACATGATCTAGCGCTGTGCGTA 434
 QY 821 TGTATGACTTAGTGGCGCAGCTAACCGCATATAGTAGACCGCTGGGAGTACGGCCGA 880
 Db 433 TCGACCCGTCAGTCTCTAGCTAACGAGTTAAGTATCCCGCTGGGAGTACGTTCCGA 374
 QY 881 AGGTAAATCAATGATGATGAGCGGGGGCCCGACAAAGGGGTGAGCATGTGTTAAT 940
 Db 373 AGAATGAACCTCAAGGAAATGACGGGGGCCCGACAAAGGGGTGAGCATGTGTTAAT 314
 QY 941 TCGAAGCAGCGGAGAACTTACTACTCTTTCACATCCACAGACATTTGAGAGATCAG 1000
 Db 313 TCGATGCAAGGAGAACTTACTTACAGGCGTTGACATCCGCCAATCTTTGAAAGAA 254
 QY 1001 ATGTGCTCTTGGGAACTGTGAGACAGGTGCTGATGCTGTGCTGACGCTGTGTTGA 1060
 Db 253 GGGGTGCTCTGGGAAACCGGACACAGGTGTGATGCTGTGCTGACGCTGTGCGCTAA 194
 QY 1061 AATGTGGGTAAATGCTCCGCTAACGAGCGCAACCTTGTCCCTTATTTTCCAGCAGTAA 1120
 Db 193 GGTGTGGGTAAATGCTCCGCTAACGAGCGCAACCTTGTCCCTTATTTTCCAGCAGTAA 136
 QY 1121 GTGGAACTTTAAGAGAGATGCTCCGCTGACAAACCGGAGAAAGTGGGAGCAGCTCAAGT 1180
 Db 135 TTTGGAACCTTGAACAGACTGCCGATTAAGCCGAGAAAGTGAAGATGAGCTCAAGT 76
 QY 1181 CATCATGCCCCCTTAAGATTAAGGCTTACACAGTCTCAATAGCGCTTACAGAGGCTCG 1240
 Db 75 CATCATGCCCCCTTAAGATTAAGGCTTACACAGTCTCAATAGCGCGGACAAAGGCTCG 16
 QY 1241 AAGCTAGCGATAGTG 1255
 Db 15 GATCCCGGAGGGTG 1

RESULT 5
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 LOCUS BOMKA47TF BO_2_3 KB Brassica oleracea genomic clone BOMKA47,
 DEFINITION genomic survey sequence.
 ACCESSION BH705272 GI:18787746
 VERSION BH705272.1 GI:18787746
 KEYWORDS
 SOURCE
 ORGANISM
 Brassica oleracea
 Brassica oleracea
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 ; euroside II; Brassicales; Brassicaceae; Brassica.
 1 (bases 1 to 1079)
 Towner, C.D., Van Aken, S., Utebback, T., Koo, H. and Fraser, C.M.
 Whole genome shotgun sequencing of Brassica oleracea
 Unpublished
 Other GSSs: BOMKA47TR
 CONTACT: Chris Town

TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA.
 Tel: 301-838-3523
 Fax: 301-838-0208
 Email: cdtown@tigr.org
 DNA is from a doubled haploid provided by Tom Osborn.
 Seq primer: TF
 Class: sheared ends.

FEATURES
 source
 Location/Qualifiers
 1..1079

/organism="Brassica oleracea"
 /mol_type="genomic DNA"
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 /db_xref="taxon:3712"
 /clone="BOMKA47"
 /clone_1="BO_2_3_KB"
 /note="Vector: pHD51; Site_1: BstXI; 2-3 kb sheared
 genomic DNA inserted into pHD51 using BstXI linkers"
 BASE COUNT 265 a 257 c 353 g 204 t

ORIGIN
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 Best Local Similarity 74.0%; Pred. No. 1,4e-164;
 Matches 805; Conservative 0; Mismatches 255; Indels 28; Gaps 3;

QY 174 GAAGAGAGGAGGACTCTTCCGAGGCTTCCGCTATTAATAGAGCTGGGTAGATTAAGTCTG 233
 Db 17 GTAGGCTGAAGAGCAATATAGAGAAATCCGCCAGAGAGAGGAGGCTCGGCTGTGATTAGCTAG 76
 QY 234 TTGGTAGAGGTAAGAGCCCTTACCAAGGCAAGATCTTACTGTGCTGAGAGATGACAGT 293
 Db 77 TTGGTAGAGCAATATGCTTACCAAGGCAAGATGATAGTGTGCTGCTGAGAGATGATCAG 136
 QY 294 CACACTGGGACTGAGACACGCGCCAGACTCTTACGAGGAGCAGCAGTGGGAAATATTGA 353
 Db 137 CACACTGGGACTGAGACACGCGCCAGACTCTTACGAGGAGCAGCAGTGGGAAATTTTCCG 196
 QY 354 CAATGGGCGGCAAGCTGATCCAGCCATGCGCGGTGTGTGAAGAGGCTTATAGGTTGTAA 413
 Db 197 CAATGGGCGAAGCTGTACGAGCAATGCGCGGTGTGTGAAGAGGCTTATAGGTTGTAA 256
 QY 414 AGCACTTTCAGGGGTGAGAGAGGATGATAGCTTAATACGTATCATCTTACGTTAGCC 473
 Db 257 ACTTCTTTTCCAGAGAGAGAG-----CAATGACGATATCTG 293
 QY 474 CAGAGAGAGACCGGCTTAATCTGTCCAGACCGCGGTAAATACAGAGGTCGAAGCGT 533
 Db 294 GGGAAATAGCACTGGCTTACTGTGTCCAGACCGCGGTAAATACAGAGGTCGAAGCGT 353
 QY 534 TAATCGAATTAATCTGGCGTAAAGCGCGCTAGAGTGTGTTAATCGATGATGTAATC 593
 Db 354 TATCCGAAATGATTTGGCGTAAAGCGCTGTAGTGTGTTAATCGCGCTGAATTC 413
 QY 594 CCAAGGCTCAACTTGGAAATGCAACCGATCTGCTAGTATGATGTGAGAGGCTG 653
 Db 414 CCAGGCGTCAACCTTGGACAGCGGTGGAATCTTCAACCACTTGAATGATGATGAGGCGACA 473
 QY 654 TGAATTTCTGCTGTAGCGGTGAATGCGTAGATTAAGAGGAAATCATGATGGCGAAG 713
 Db 474 GGGAAATTTCCGCTGAGCGGTGAATGCGTAGATTAAGAGGAAATCATGATGGCGAAG 533
 QY 714 CGAACCCTGCAATTAATCTGAACCTGAGGTGCGAAGCGTGGGAGCAACAGATTAG 773
 Db 534 CACTCTGCTGGCGCACTAGCACTGAGAGAGGAAGGTAGGGGAGCAATGGGATTAG 593
 QY 774 ATACCTGATGATCCAGCGGTAACGATGCTACTAGCGCTG---GGTGAATGACT 830
 Db 594 ATACCCAGATGATCTTACCGGTAAACGATGATTAAGGCGCTGTGCTGATGACCCGTG 653
 QY 831 TAGTGGCGAGCTAACCAATTAATAGACCGCTGGGAGATACGCGCGCAAGATTAAAC 890
 Db 654 CAGTGTGTAGCTTAAGCGTTAATGATCCCGCTGGGAGATAGCTTCGCAAGATGAAC 713
 QY 891 TCAATGATTAATGAGGGGGGCCGACAGAGGTGAGCATGTGCTTATTTGAAGCAAC 950
 Db 714 TCCAGGAATTAAGAGGGGGGCCGACAGAGGTGAGCATGTGCTTATTTGAAGCAAC 773
 QY 951 GCGAAGAACCTTACCTTCTTGAATCCACAGACATTTGAGAGATGAGATGTGCTT 1010
 Db 774 GCGAAGAACCTTACCAAGGCTTGAATCCCGGCAATCTCTTGAAGAGAGGGGTCTT 833
 QY 1011 CGGAACTGTGAGACAGGTGCTGATGCTGTGTAGCTGTGTGTTGTAATGTTGGGT 1070
 Db 834 CGGAAAGCGGAGACAGGTGCTGATGCTGTGTAGCTGTGTGTTGTAATGTTGGGT 893
 QY 1071 TAACTCCGTAACGAGGCAACCTTGTCTTATTTGCAAGCAGTAAATGTTGGAACTT 1130
 Db 894 TAACTCCGTAACGAGGCAACCTTGTCTTATTTGTTAGTCCAA--CCGTGATTTGGAACC 951
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QY 1191 CTTACGAGTATGGGCTTACACAGCTGCTACATAGCGCTATACAGAGGCGCTGCAAGTACGGA 1250
 DB 1012 CTTATGCGCTTGGGCGACACAGCTGCTATCATGCGCGGACAAAGGCTGCGATCCCGGA 1071
 QY 1251 TAGTGAGC 1258
 DB 1072 GGGTGAGC 1079

RESULT 6
 BZ463550/c
 LOCUS BZ463550 1044 bp DNA linear GSS 13-DEC-2002
 DEFINITION BONK86TF BO.1.6.2 KB for Brassica oleracea genomic clone BONK86,
 genomic survey sequence.

ACCESSION BZ463550
 VERSION BZ463550.1 GI:26749465
 KEYWORDS GSS.
 SOURCE Brassica oleracea
 ORGANISM Brassica oleracea
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 / eurosids II; Brassicales; Brassicaceae; Brassica.
 1 (bases 1 to 1044)
 Town,C.D., Van Aken,S., Uteback,T., Koo,H. and Fraser,C.M.
 Whole genome shotgun sequencing of Brassica oleracea
 Unpublished
 Other_GSSs: BONK86TR
 CONTACT: Chris Town

REFERENCE 1179
 TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA.
 Tel: 301-838-3523
 Fax: 301-838-0208
 Email: cdtown@tigr.org
 DNA is from a doubled haploid provided by Tom Osborn.
 Seq primer: TP
 Class: sheared ends.

FEATURES
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 Location/Qualifiers
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 /db_xref="taxon:3712"
 /clone="BONK86"
 /clone_1b="BO.1.6.2 KB tot"
 /note="Vector: pHOSt1; Site 1. BactX1; 1.6-2 kb sheared
 total DNA inserted into pHOSt1 using BactX1 linkers"
 BASE COUNT 199 a 327 c 261 g 257 t

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 Matches 760; Conservative 0; Mismatches 221; Indels 6; Gaps 3;

QY 462 TGAAGTAAAGCCGGAAGAGCAACGAGTAACTCTGTCAGAGAGCGCGGTATATACGA 521
 DB 999 TGAAGTAAAGCCGGAAGAGCAACGAGTAACTCTGTCAGAGAGCGCGGTATATACGA 940
 QY 522 GGGTGAAGCGTTAATCGAATTAAGTGGCGTAAAGCGCGGTAGTGTGTTGAATC 581
 DB 939 GATGCAAGCGTTAATCGAATTAAGTGGCGTAAAGCGGTAGTGTGTTGAATC 880
 QY 582 GATGCAAGCGTTAATCGAATTAAGTGGCGTAAAGCGGTAGTGTGTTGAATC 641
 DB 879 GCGCGTAAATCCAGAGGCTCAACCTTGAAGAGCGCGGTAGTGTGTTGAATC 820
 QY 642 GGTAGAGGAGTGTGAATTTCTGTAGAGCGGTGAATCGTGAATATAGGAAGAACAT 701
 DB 819 GGTAGAGGAGTGTGAATTTCTGTAGAGCGGTGAATCGTGAATATAGGAAGAACAT 760
 QY 702 CAGTGGGAAGCGCAACCTTGACATTAATCTGACACTAGAGCGGAAGCGTGGGAGC 761
 DB 759 CAAAGCGGAAGCGCAACCTTGACATTAATCTGACACTAGAGCGGAAGCGTGGGAGC 700

QY 762 AACACGATTAATACCTCGTGAAGTCCACGCGCGTTAAAGATGTCTACTAGCCGTG--G 818
 DB 699 GAATGGATTAATACCTCGTGAAGTCCACGCGCGTTAAAGATGTCTACTAGCCGTGCG 640
 QY 819 GTTGTAAATGACTTAAGTGGCGAGCTAAGCAATTAAGTGAACCGCGTGGGAGTACGACCG 878
 DB 639 TATGACCCCGGAGTGTGCTAGCTAAGCTTAAAGTATCCCGCTGGGAGTACGTTCC 580
 QY 879 CAAAGTAAACTCAATGAATTAAGTGGCGAGCTAAGCAATTAAGTGAACCGCGTGGGAGT 938
 DB 579 CAAAGTAAACTCAATGAATTAAGTGGCGAGCTAAGCAATTAAGTGAACCGCGTGGGAGT 520
 QY 939 ATTGGAAGAGAGCAAGCAATTAAGTGGCGAGCTAAGCAATTAAGTGAACCGCGTGGGAGT 998
 DB 519 ATTGGAAGAGAGCAAGCAATTAAGTGGCGAGCTAAGCAATTAAGTGAACCGCGTGGGAGT 460
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 DB 459 GAGGGGTGGCTTGGGAACTGTGAGACAGTGTGCAATGCTGTGCTGCTGCTGCTGCTGCT 400
 QY 1059 GAATGGTGGCTTGGGAACTGTGAGACAGTGTGCAATGCTGTGCTGCTGCTGCTGCTGCT 1118
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 DB 341 AGTGGAACTTAAAGAGAGTGTGAGACAGTGTGCAATGCTGTGCTGCTGCTGCTGCTGCT 282
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 DB 281 GTTCATCATGCGCTTACAGATGAGTGGCTTACAGAGTGTGCAATGCTGTGCTGCTGCT 222
 QY 1239 GCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1298
 DB 221 GCGATCCCGGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 162
 QY 1299 AACTGACATTCATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1357
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 QY 1358 AGTTCCCGGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1417
 DB 101 TCGTTCCCGGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 42
 QY 1418 AGCTAGCTTAACCTTCCGAGATGGCG 1444
 DB 41 CGTTACTTAACCGCAAGAGGAGGAGG 15

RESULT 7
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 DEFINITION BONH54TR BO.1.6.2 KB for Brassica oleracea genomic clone BONH54,
 genomic survey sequence.
 ACCESSION BZ494182
 VERSION BZ494182.1 GI:27004681
 KEYWORDS GSS.
 SOURCE Brassica oleracea
 ORGANISM Brassica oleracea
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 / eurosids II; Brassicales; Brassicaceae; Brassica.
 1 (bases 1 to 1051)
 Town,C.D., Van Aken,S., Uteback,T., Koo,H. and Fraser,C.M.
 Whole genome shotgun sequencing of Brassica oleracea
 Unpublished
 Other_GSSs: BONH54TR
 CONTACT: Chris Town
 TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA.
 Tel: 301-838-3523
 Fax: 301-838-0208

Email: cdtown@ligr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends

FEATURES
Source Location/Qualifiers

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/mol_type="genomic DNA"
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total DNA inserted into pHOSt using BstXI linkers"
BASE COUNT 202 a 332 c 259 g 258 t
ORIGIN

Query Match 39.8%; Score 591.4; DB 29; Length 1016;
Best Local Similarity 77.0%; Pred. No. 8.1e-164;
Matches 760; Conservative 0; Mismatches 221; Indels 6; Gaps 3;
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999 TGACGCTATCTGGGGAATTAACCATCGCTAACTGTGCGACAGCCGCGTAATACAGA 940
522 GGGTGCAGACGCTTAATCGGAATTACTGCGCGTAAAGCGCGGTAGTGTGTAAAGTC 581
939 GGATGCAAGCGTTATCCGGATGATTTGGCGTAAAGCGTGTAGAGTGGCTTTTAAATC 880
582 GGATGCAAGCGTTATCCGGATGATTTGGCGTAAAGCGTGTAGAGTGGCTTTTAAATC 641
879 CGCCCTCAATCCAGGCTCAACCTCGGACAGCGGTGAAACTCCAGCTTGAATC 820
642 GGTAGAGGGGTGTGAATTTCTGTGTAGCGGTGAATTCGTAGATTAAGAAAGAACT 701
819 GGTAGAGGGCAAGGGAATTTCCGCTGAGCGGTGAATTCGTAGATTAAGAAAGAACT 760
702 CAGTGGCGAAGCGCAACCTCGGCTAACTGACACTGAGCGGCAAGCGGTGGGAGAC 761
759 CAACGCGAAGCACTCTGCTGGGCGACACTGACACTGAGCAAGCAAGCTTGGGAGAC 700
762 AAAGAGATTAGATACCTGTGTAAGTCCAGCCGTAACGATGTCTACTAGCCGTTG--G 818
699 GAATGGATTAGATACCTGTGTAAGTCCAGCCGTAACGATGTCTACTAGCCGTTG 640
819 GTTGTATGACTTGTGTGCGCACTTAACGAATTAAGTACCGCCCTGGGAGTACGCCG 878
639 TATGACCCCGTGAAGTGTGTGTAAGTATCCCGCTGGGAGTACCGCTTG 580
879 CAAGTTAAACTCAATGAATGACGCGGCGCGCAAGCGGTGAGCATGTGTTA 938
579 CAAGATCAAACTCAAGGAATTAACGCGGCGCGCAAGCGGTGAGCATGTGTTA 520
939 ATTGGAAGCAAGCGGAAGAACCTTACTCTTGAATCAAGCAAGCAATTGAGAGATC 998
519 ATTGGAAGCAAGCGGAAGAACCTTACTCTTGAATCAAGCAAGCAATTGAGAGATC 460
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1179 GTCAATGAGCCCTTACAGAGTGGGCTACACAGTGTGCAATGAGGATTAAGAGAGCT 1238
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QY 1239 GCAAGTAGCGATAGTAGAGGATCCACAAATACGTGTAGTCCGATGGAGTCTC 1298
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QY 1299 AACTCGACTCCATGAAAGTGGAAATCCCTAGTAATGCTGAATGAG-AATGTACAGTGAAT 1357
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QY 1358 ACGTTCGCGGCGCTTGTACACACCGCGCTCACCATGAGGAGTGTATGCTCCAGAGT 1417
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DEFINITION BOND228Tf BO_1.6.2_KB_tot Brassica oleracea genomic clone BOND228,
Genomic survey sequence.
ACCESSION B2426201
VERSION B2426201.1 GI:26667713
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
1 (bases 1 to 1016)
REFERENCE Town,C.D., Van Aken,S., Uterback,T., Koo,H. and Fraser,C.M.
Whole genome shotgun sequencing of Brassica oleracea
TITLE Unpublished
JOURNAL Other GSSs: BOND228Tf
COMMENT Contact: Chris Town
TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@ligr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TF
Class: sheared ends.

FEATURES
Source Location/Qualifiers

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/clone="BOND228"
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/note="Vector: pHOSt; Site 1: BstXI; 1.6-2 kb sheared
total DNA inserted into pHOSt using BstXI linkers"
BASE COUNT 193 a 328 c 239 g 256 t
ORIGIN

Query Match 39.7%; Score 590.4; DB 29; Length 1016;
Best Local Similarity 76.0%; Pred. No. 1.6e-163;
Matches 792; Conservative 0; Mismatches 221; Indels 29; Gaps 4;
QY 212 GAGCGTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 271
DB 1016 GGGGTGGGCTGATTAAGTGTAGTGGTGAAGCAATGATGATGATGATGATGATGATGAT 957
QY 272 CTGCTGAGAGATGACCAATGACACTGGAATGAGACAGCGCCCAAGCTCTTACGGGA 331
DB 956 CTGCTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 897
QY 332 GCGAGAGTGGGATATGACCAATGAGCGGAGAGCTGATGATGATGATGATGATGATGAT 391
DB 896 GCGAGAGTGGGATATGACCAATGAGCGGAGAGCTGATGATGATGATGATGATGATGAT 838


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QY 392 GAAGAAAGCCTTAGGTTGTAAGACCTTCAGGGGTGAGGAAGGTGATAGTTAATAC 451
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QY 452 GTATATCTTTGAGCTTACCCCGAGAGAGACCGCTAACTCTGTGCCAGACCGCG 511
DB 793 -----CATGACGGTATCTGGGGAATAGCATCGCTTACTGTGTCCAGACCGCG 741
QY 512 GTATATCAGAGGGGTGAAAGCCTTAACTGGAATTAATCTGGCGCTAAAGCGGCTGTGT 571
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 genomic survey sequence.
 ACCESSION
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 VERSION
 BH656222.1 GI:18714532
 KEYWORDS
 GSS.
 SOURCE
 ORGANISM
 Brassica oleracea
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliopsida; eudicotyledons; core eudicot; rosids

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REFERENCE ; euroids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 1031)
AUTHORS Town,C.D., Van Aken,S., Uterback,T., Koo,H. and Fraser,C.M.
TITLE Whole genome shotgun sequencing of Brassica oleracea
JOURNAL Unpublished
COMMENT Contact: Chris Town
TIGR
912 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TF
Class: sheared ends.
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Query Match 39.7% Score 589.8; DB 28; Length 1031;
Best Local Similarity 74.9%; Pred. No. 2,4e-163;
Matches 790; Conservative 0; Mismatches 227; Indels 28; Gaps 3;
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QY 380 TGCCGCGGTGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 439
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QY 440 ATAGTTAATAGTTATCATCTTACGTTAGCCCCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 499
DB 915 -----CATGACGATCTGGGGAATAGCATGCGTAACTCTGTG 875
QY 500 CAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 559
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QY 740 GAGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 799
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QY 800 GATGTCTACTAGCGGTTG---GGTGTATAGCTTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 856
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QY 857 GACCGCTGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 916
DB 514 TCCCGCTGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 455
QY 917 AAGCGTGTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 976

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 QY 1037 GGCTGTGTGAGCTCGGTGTGTGAAAATGTGGTGTAAAGTCCGTAAACAGGCAACCTT 1096
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 QY 1217 ACAATGGCGTATACAGAGGCTGCAAGCTAGCATAGAGCGAAATCCACAAAGTACGT 1276
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 QY 1277 CGTAGTCCGATTTGAGACTCTGCACTGCACTGCACTGCACTGCACTGCACTGCACT 1336
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RESULT 10
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 LOCUS CD042372.1 GI:30495965
 DEFINITION psHB040x24f_302263 psHB: Infected hypocotyl soybean host. 48 hrs post infection Phytophthora sojae cDNA clone psHB040F24 5. mRNA

ACCESSION CD042372
 VERSION CD042372.1 GI:30495965
 KEYWORDS EST.
 SOURCE Phytophthora sojae
 ORGANISM Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae; Phytophthora.

REFERENCE 1 (bases 1 to 741)
 AUTHORS Tyler, B.M., Udelsom, H.S., Gjisen, M., Dean, R.A. and Waugh, M.E.
 TITLE USDA-IPAFs: Expression of Phytophthora sojae genes during infection and propagation

JOURNAL Unpublished
 COMMENT Contact: Tyler B
 Tyler Lab

VBI
 1880 Pratt Dr., Blacksburg, VA 24061, USA
 Tel: 540-231-7318
 Email: bmtyle@vt.edu
 PCR Primers
 FORWARD: BK reverse
 Plate: 040 row: F column: 24
 Seq primer: BK reverse
 High quality sequence stop: 741.
 Location/Qualifiers

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 Query Match 39.6%; Score 588.6; DB 14; Length 741;
 Best Local Similarity 88.8%; Pred. No. 4.5e-163;
 Matches 659; Conservative 0; Mismatches 80; Indels 3; Gaps 2;

QY 366 GCTGATCCAGCATGCGCGGTGTGTGTAAGAGAGGCTTTAGGTTGTAAGCATTTGACG 425
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 QY 426 GGTGAGAGAGGATAGATTATATAGTATCATCTTACAGTTAGCCCAAGAGAGAC 485
 Db 681 GG-GAGAGAGGCTTACAGAGAAATACGTGTAGTTTACCTTACCCAGAGATTAAGAC 623
 QY 486 CGGCTACTCTGTGCCAGACGCGCGGTATATACAGAGGGTCCAAAGCTTAATCGAAATTA 545
 Db 622 CGGCTAACTTCTGTGCCAGACGCGCGGTATATACAGAGGGTCCAAAGCTTAATCGAAATTA 563
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 QY 606 CTGGAGATGCAACCGGATCTGCTAGCTAGAGTATGATAGAGGGTGTGAATTTCTG 665
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 QY 666 TGTAGGTGTGAATATGCTATATATAGAGAAATCATGTGCGAAGGCGCACCTTGA 725
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 QY 786 TCCAGCCGCTAAACGATGCTTACTAGCCGTTGGTT--GTATGACTTATGTGCGCACT 843
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 QY 844 AACGCAATAGTAGACCGGCTGGGAGTACGGCGCAAGGTAAATCAATGAATGA 903
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 QY 904 CGGGGGCCGCAACAAGCGGTGAGCATGTGTTTATTCGAGCAACCGGAACCTTA 963
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 QY 1084 GAGCGCAACCTTGTCTTATT 1105
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RESULT 11
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 genomic survey sequence.
 ACCESSION BZ450751
 VERSION BZ450751.1 GI:26721334
 KEYWORDS GSS.
 SOURCE Brassica oleracea
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids

REFERENCE : eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 1077)
AUTHORS : Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M.
TITLE : Whole genome shotgun sequencing of Brassica oleracea
JOURNAL : Unpublished
COMMENT : Other GSSs: BONB063TF
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.

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total DNA inserted into pHD01 using BstXI linkers"

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Best Local Similarity 76.9%; Pred. No. 9.6e-163;
Matches 757; Conservative 0; Mismatches 222; Indels 6; Gaps 3;

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QY 522 GSGTGCAGCGTTAATCGGAATTAAGTCTGTGTCACGACCGCGGTAAATAGTC 581
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Db 189 GCGGCTCAATCCCAAGGCTCAACCTGACGACGCGGTGGAATTAAGTCTGTGTCACG 248
QY 642 GGTAGAGGGGTGTGAATTTCTGTGTCACGCGTGAATTCGTGTAATAGAGAGAAAT 701
Db 249 GGTAGAGGGGTGTGAATTTCTGTGTCACGCGTGAATTCGTGTAATAGAGAGAAAT 308
QY 702 CAGTGGCGAAGGGAACCTCTGATTAATTAAGTCTGTGTCACGCGTGAATTCGTGTAAT 761
Db 309 CAGTGGCGAAGGGAACCTCTGATTAATTAAGTCTGTGTCACGCGTGAATTCGTGTAAT 368
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Db 489 CAAGGTTAAATCAATGATTAAGTCTGTGTCACGCGTGAATTCGTGTCACGCGTGAATTCGT 548
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Db 669 AAGGTTGGGTTAAGTCCGTAAAGAGGCAACCTTGTCTTAATTTGCAAGACAGTTAA 726
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Db 727 AGTTGGAAGACTTAAGAGAGTCTGCGGTGACCAACCGGAGAGGTGGGACAGCTCA 786
QY 1179 GTGATATGAGGCTTACGAGTGAAGGCTTACACAGTGTCTTAATGCGGTATACAGAGGCT 1238
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QY 1358 AGCTTCCCGGAGGCTTACGAGTGAAGGCTTACACAGTGTCTTAATGCGGTATACAGAGT 1417
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DEFINITION
Genomic survey sequence.
ACCESSION B2685785
VERSION B2685785.1 GI:28245311
KEYWORDS
GSS.

SOURCE
ORGANISM
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 899)
REFERENCE
White, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick
A., Fraser, C.M., Juan, Y., San Miguel, F., Ma, J. and Benneken, J.
TITLE
Maize Genomics Consortium
JOURNAL
Unpublished
COMMENT
Contact: Cathy White

TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: white@tigr.org
Seq primer: TP
Class: sheared ends.

FEATURES
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Query Match 38.8%; Score 576; DB 29; Length 899;
Best Local Similarity 80.0%; Pred. No. 2.7e-159;
Matches 728; Conservative 0; Mismatches 155; Indels 29; Gaps 4;
QY 331 AGGACGAGTGGGGAATTTGACATGAGGGAAGAGCTTATCAGGCAATCCGCGGTG 390

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Db      899 AGGAGCAGTGGGGAAATTGGACAATGGGGCGCAAGCCTGATCCAGCCATGCCCGCTGAG 840
Qy      391 TGAAGAAAGCCTTAGGGTTGTAAGCACTTTAGAGGGGTGAGAAAGGTGATAGTTAATA 450
Db      839 TGAATGAAGCCTTAGGGTTGTAAGCCTT-----TTTGTG 805
Qy      451 GGTATCATCTTTAGCTTAAAGCCCAAGAAAGACCGGCTTAACCTCTGTGCAAGACCGC 510
Db      804 CGGACGATTAATGACGGTACCGGAAGATAAGCCCGGCTAACTTCTGTGCAAGACCGC 745
Qy      511 GGTATTAACAAGGGGCGCAAGGCTTAATCCGAATTAAGCTGGGGCTTAAGCGGGTAGTGG 570
Db      744 GGTATTAACAAGGGGCGCTAAGCTTCTGTGCAAGCTGGGGCTTAAGCGGGTAGTGG 685
Qy      571 TTTGTTAAGTCGATGTTGAAATCCAGGGCTCAACCTTGGATGGAACCCGATATCGCT 630
Db      684 CCATTCAGTCGGGGGTGAAGCTGTGCTCAACACAGAAATTCCTTCGATATCGTTT 625
Qy      631 AGCTAGATATGATGATGAGGGGTGTAATTTCCGTGTACCGGTGAATTCCTATATATA 690
Db      624 GGTGATGATTTGATGATGAGGTGTTGTGGAATGCGAGGTGATGAGGTGAATTCGATATAT 565
Qy      691 GGAAGAAACATCAGTGGCGAAGCGACACCTTGACTAATATGACACTGAGGTGCGAA 750
Db      564 CGAAAGAACACAGTGGCGAAGCGCGCACTGGAACCAACACTGACGCTGAGGCGGAA 505
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Qy      811 GCCGTTGGGTTG-TAATGACTTATGAGGGCGAGCTTAACGAATTAAGTAAAGCCGCTGGGA 869
Db      444 GCTGTGGGGTGTCTGACCTCAGTACGCGAGCTTAAGCCTTTAAGCATTCGCTTGGGA 385
Qy      870 GTACGCGCGCAAGGTTAAACTCAATGAATTAACGCGGCGCGCAACAGCGTGAAGA 929
Db      384 GTACGCGTGCAGAAATTAAACTCAAGGAATTAACGCGGCGCGCGCAACAGCGTGAAGA 325
Qy      930 TGTGTTAATTTCAAGAGACGCGAAGACCTTAACCTTACTTGAACATCCAGAACAT 989
Db      324 TGTGTTAATTTCAAGAGACGCGAAGACCTTAACCTTACTTGAACATTCGTCGATCC 265
Qy      990 TGAAGATCAGATGATGCTTCCGGAACCTGTAAGACAGGTGCTGACAGCTGTGCTGAC 1049
Db      264 GGAAGATCCGGGGTTCCTTCGGGGAACGGAACAGGTGCTGACAGCTGTGCTGAC 205
Qy      1050 TCGTGTGTTGAATGTTGGGTTAAGTCCCTTAACGAGCGCAACCTTGTCTTATTTGCC 1109
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Qy      1110 AGCAGTATGATGATGAGAACTTTAAGAGACTGCGCGGTGACAAACG-GAGGAAGTGGAG 1168
Db      144 ATCA--TTCAATTTGGGCACTCTAGAGAGACTGCGCGGTGATTAACCGCGAGGAAGTGG 87
Qy      1169 ACGAGTCAAGTCAATCATGATGCTTACAGAGTGAAGGCTTACACAGTGTCTACATGGCTAT 1228
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RESULT 13
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LOCUS      BH647750/c
DEFINITION  BOMND31TR BO.2.3 KB Brassica oleracea genomic clone BOMND31,
ACCESSION  BH647750
VERSION    BH647750.1 GI:18705298
KEYWORDS   GSS.
SOURCE     Brassica oleracea
ORGANISM   Brassica oleracea

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REFERENCE
AUTHORS    Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
TITLE      Whole genome shotgun sequencing of Brassica oleracea
JOURNAL    Unpublished
COMMENT    Contact: Chris Town
TIGR       9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.
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/strain="TO1000D3"
/db_xref="taxon:3712"
/clone.lib="BO.2.3 KB"
/notes="vector: pHOSt; Site 1: BstXI; 2-3 kb sheared genomic DNA inserted into pHOSt using BstXI linkers"
BASE COUNT  201 a 334 c 263 g 256 t
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Query Match 38.5%; Score 571.6; DB 28; Length 1054;
Best Local Similarity 76.7%; Pred. No. 6e-158;
Matches 765; Conservative 0; Mismatches 224; Indels 9; Gaps 5;

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Qy      480 AAGCAGCGCTTAACCTGCTGACGAGCGCGGTAAATACAGAGGTGCAAGCTTAATCG 539
Db      1054 AAGCATCGCTTAACCTGCTGACGAGCGCGGTAAATACAGAGGTGCAAGCTTAATCG 995
Qy      540 GAATTAATGAGGCGTAAGAGCGCGGTGATGTTGTTAAGTGAATGCCAGAG 599
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Qy      600 CTCACCTTGAATGACACCCGATGCTGCTAGTGAATGATGATGATGATGATGAT 659
Db      935 CTCACCTTGAATGACACCGGTGTAATCAAGCTTGAATGATGATGATGATGATGAT 876
Qy      660 TTCCGTGATGCGGTGAATGCTGATGATGATGATGATGATGATGATGATGATGAT 719
Db      875 TTCCGTGATGCGGTGAATGCTGATGATGATGATGATGATGATGATGATGATGAT 816
Qy      720 CTTGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 779
Db      815 GCTGAGGCGCACTGACACTGAGAGAGAAAGCTAGAGAGAGAGAGAGAGAGAGAGAG 756
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Db      755 CAGTATGCTGAGCGGTGAATGATGATGATGATGATGATGATGATGATGATGAT 696
Qy      837 CGCAGCTAAGCAATAGTGAACCGCTGAGAGTACGCGCGCAAGTTAAATCAAT 896
Db      695 TGTAGCTAAGCGGTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 636
Qy      897 GAATTAAGCGGGGCGCGACAGCGGTGATGATGATGATGATGATGATGATGATGATGAT 956
Db      635 GAATTAAGCGGGGCGCGACAGCGGTGATGATGATGATGATGATGATGATGATGATGAT 576
Qy      957 AACCTTACTTCTTGAATCAAGCAATTTGAGATGATGATGATGATGATGATGATGAT 1016
Db      575 AACCTTCAAGGCTTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 516
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Db      515 CGCGACACAGGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 456

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QY 1077 CCGTAACGAGCGACCCCTTCTTATTTGCCAGACGTATGTGGAACTTTAAGA 1136
 DB 455 CCGCAACGAGCGAACCCCTCGTGTAGTTGCCA--CCGTGAGTTTGAACCTGAA 398
 QY 1137 GACTGCCGCTGACAAACCCGAGAGAGTGGAGACAGCTCAATCATATGAGCCCTTACG 1196
 DB 397 GACTGCCGCTGACAAACCCGAGAGAGTGGAGAGTCAATCATATGAGCCCTTACG 338
 QY 1197 AGTAGGCTTACACAGCTGTCTACATGCGCTATACAGAGGCTGCAAGCTAGCATAGTA 1256
 DB 337 CCCTGGGCGACACACCGGTCTACATGCGCGGCAAGAGGTGCGATCCCGAGAGGTGA 278
 QY 1257 GCGAATCCCAAAAGTACGTCTATGTCGGATTTGAGAGTGTGCAATTGCACTTCAATGAGT 1316
 DB 277 GCTAATCTCAAAAACCCGCTTCAATGCTGATTTGAGAGTGTGCAATGCTTCAATGAGT 218
 QY 1317 CCGAATCGCTAGTAACTGTTGATCAG--AATGTACCGGTGATATCTTCCGGGCTTGT 1375
 DB 217 CCGAATCGCTAGTAACTGTTGATCAG--AATGTACCGGTGATATCTTCCGGGCTTGT 158
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 DB 157 CACACCGCCCGTCAACACCATGGAGTTGATTTGCTCAGAGTACTAGCTTAACCTTTCG 1400
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RESULT 14
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 BZ440868
 VERSION BZ440868.1 GI:26598161
 KEYWORDS GSS.
 SOURCE Brassica oleracea
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 1 (bases 1 to 974)
 REFERENCE Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
 Whole genome shotgun sequencing of Brassica oleracea
 Unpublished
 JOURNAL Other GSSs: BONKTS1TF
 COMMENT Contact: Chris Town
 TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA.
 Tel: 301-838-3523
 Fax: 301-838-0208
 Email: cdtown@tigr.org
 DNA is from a doubled haploid provided by Tom Osborn.
 Seq primer: TR
 Class: sheared ends.

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 total DNA inserted into pHSI1 using BstXI linkers"

BASE COUNT 245 a 227 c 314 g 188 t
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Query Match 36.1%; Score 566.2; DB 29; Length 974;
 Best Local Similarity 76.4%; Pred. No. 2,3,5,156;
 Matches 746; Conservative 0; Mismatches 203; Indels 28; Gaps 3;

QY 250 CTACCAAGCGACGATCTCTTAATCTGTCTGAGAGATGACCACTGCGATCGAGA 309
 DB 17 CTTACAGGCGCATGATCATAGTCTGTCCGAGAGATGATCAGACACTGGGACTGAGA 76
 QY 310 CAGGCCCAAGACTCCTTAAGGAGGAGAGAGAGGAGGAAATTATGGAACAATGGGCGACGCT 369
 DB 77 CAGGCCCAAGACTCCTTAAGGAGGAGAGAGAGGAGGAAATTATGGAACAATGGGCGACGCT 136
 QY 370 GATCCAGCCATGCGCGGTGTGTGAAGAAAGCCCTTAAGGTTGAAGCACTTTCAGGGGTG 429
 DB 137 GACGAGCAATGCGCGGTGTGTGAAGAAAGCCCTTAAGGTTGAAGCACTTTCAGGGGTG 156
 QY 430 AGGAAGGATGATAGGTTAATACGTATCATCTTGAACCTTGAAGCCCAAGAGACCGGC 489
 DB 197 AAGAG-----CAATACCGATCTGGGGAATGAATGATGAC 253
 QY 490 TAATCTGTGCGAGCAGCGCGGTATATACAGAGGTTGCAAGCTTAATCGAAATTACTGG 549
 DB 234 TAATCTGTGCGAGCAGCGCGGTATATACAGAGGTTGCAAGCTTAATCGAAATTACTGG 293
 QY 550 GCGTAAAGGCGCGGTAGTGTGTGTGAAGAAAGCCCTTAAGGTTGAAGCACTTTCAGGGGTG 609
 DB 294 GCGTAAAGGCGGTAGTGTGTGTGAAGAAAGCCCTTAAGGTTGAAGCACTTTCAGGGGTG 353
 QY 610 GATGAGCAAGCGATCTGCTAGCTAGAGTATGATAGAGGAGTGTGAATTTCTGTGA 669
 DB 354 GATGAGCAAGCGATCTGCTAGCTAGAGTATGATAGAGGAGTGTGAATTTCTGTGA 413
 QY 670 GCGGTGAATGCGGTATATGAGAAAGAACTTCTGCGAGGCGACACCTTGTGACTAA 729
 DB 414 GCGGTGAATGCGGTATATGAGAAAGAACTTCTGCGAGGCGACACCTTGTGACTAA 473
 QY 730 TACTGACCTGAGTGTGCGAAAGCGTGGGAGCAACAGAGTTAGATCCTGTGATGCA 789
 DB 474 CACTGACCTGAGTGTGCGAAAGCGTGGGAGCAACAGAGTTAGATCCTGTGATGCA 533
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 DB 594 GCGTGAATGATGCGCGCTGGGAGTACGCGGAGGCGCAAGGTTAAATCTCAATGAAATGACG 653
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 DB 774 GGTGCTGATGCTGTCTGTACGCTGCTGTGTTGAAATGTTGGTTAATGCTCCGTAACGAG 833
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 DB 834 CCGAACCCTTCTCTTATTTGCGACAGATGATGTTGGGAACCTTAAGGAGATGCGCGGT 891
 QY 1147 GACAAACCGAGAGAGTGGGAGCAGCTCAAGTATCATGAGCCCTTAAGGAGGCTA 1206
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genomic survey sequence.
 accession BZ474941 GI:26776372
 version BZ474941.1
 keywords GSS.
 source Brassica oleracea
 ORGANISM Brassica oleracea
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 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 1 (bases 1 to 1069)
 town, C.D., Van Aken, S., Uterback, T., Koo, H. and Fraser, C.M.
 Whole genome shotgun sequencing of *Brassica oleracea*
 unpublished
 other GSSes: BONKR59TF
 contact: Chris Town
 TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA.
 Tel: 301-838-3523
 Fax: 301-838-0208
 Email: cdtown@tigr.org
 DNA is from a doubled haploid provided by Tom Osborn.
 Seq primer: TR
 Class: sheared ends.

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 987 -----TTTCCAGTGGCGGAGCGGCTGAGTAAACCGTGAAGATTTGCTTGTG 941
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 940 AGGGGAAACCACTGAGAAACGCTGCTAATACCCCTAGCTGAGAGGCAAA----- 887
 183 GGACTCTTGGAGCCCTTCCGCTAATAGTAGAGCTGCGTGAATAGCTAAGTTGGTAG 242
 886 -----GGAGAAATCCGCCGAGAGAGGCGCTCGGCTGATTAAGCTAGTTGAGAG 836
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 775 ACTGAGACAGCGCCAGACTCTTAAGGAGGACAGTGGGGAATATGGGCAATGGCG 716
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 715 AAAGCTGACGAGAGAAAGCGCGTGAAGAGGCTTAAAGCTTTC 656
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 655 CCAGAGAGAGAG-----CAATGACGCTATCTGGGGAATAG 619
 483 CACGAGCTAATCTGTGCGAGAGCGCGGTAATACAGAGGAGTCAAGCCTTAATCGAA 542

DB 618 CATCGGTAATCTGTGCGAGAGCGCGGCTAATACAGAGATGCAAGCTTATCCGAA 559
 QY 543 TTAATGAGCGTAAGCGCGGCTAGTGTGTTGTTAATGCGATGGAATCCAGAGCTC 602
 DB 558 TGAATGGCGTAAGAGGCTGTGTAGTGTGCTTTTAAATCGCGCAATCCAGAGCTC 499
 QY 603 AACCTGGAATGAGCAACCCGATCTGCTAGTGAATGATGATGAGAGGAGTGAATTC 662
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 QY 663 CTGTGAGCGGTGAATGCGTGAATATAGAAAGAAATCACTGAGCGAAAGGACACCT 722
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Search completed: January 30, 2004, 23:43:13
 Job time : 3503.17 secs

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Qy	193	GAGCCTTCGGCATTAAGTAGAGCTCGGTAGATTTACTGTTGAGTAAAGGTTAAAGGCTAA	252
Db	176	GGGCTTGGCATTAAGTAGAGCTTAAGTTCGATTACCTAGTTGGTAGAGTTAAATGGCTCA	235
Qy	253	CCAGGCGAGCATCTCTAACTGATCTGAGAGGATGACCACTGCACTAGGAGCTGACACAC	312
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Qy	373	CAAGCCATGCCCGGTGTGTAAGAGGCTTAGGTTGTAAACACTTTACAGGGGTGAAG	432
Db	356	CAAGCCATGCCCGGTGTGTAAGAGGCTTTCGATTGTAAACCACTTTAAAGTTGGGAAG	415

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 Db 416 AAGGSCATTAACCTAATACGTAGTGTGTTGACGTTACCGACAAATTAAGACCGGCTAA 475
 QY 493 CTCTGGCCAGAGCCGGGATATACAGAGGTCGACGCTTAATCGGAATTTCTGGGCG 552
 Db 476 CTCTGGCCAGAGCCGGGATATACAGAGGTCGACGCTTAATCGGAATTTCTGGGCG 535
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 US-09-821-016-5
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 ; Patent No. 648551
 ; GENERAL INFORMATION:
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 ; TITLE OF INVENTION: Polyhydroxyalkanoate Synthase and Gene Encoding the Same Enzyme
 ; FILE REFERENCE: 4051021
 ; CURRENT APPLICATION NUMBER: US/09/821, 016
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: Microsoft Word
 ; SEQ ID NO. 5
 ; LENGTH: 1501
 ; TYPE: DNA
 ; ORGANISM: Pseudomonas jessenii P161 ; BP-7376
 ; FEATURE:
 US-09-821-016-5

Query Match 76.1% Score 1131; DB 4; Length 1501;
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 QY 133 CATGTGAAAGCATGCTAATACCGCATACGCTTGAAGGAGGAGGAGGAGGAGGAGGAGGAGG 192
 Db 118 CGTCTGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 175
 QY 193 GAGCTTCCGCTATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 252
 Db 176 GAGCTTCCGCTATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 235
 QY 253 CCAGGCGAGCATCTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 312
 Db 236 CCAGGCGAGCATCTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 295
 QY 313 GCGCCGACCTCTTAACGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 372
 Db 296 GCGCCGACCTCTTAACGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 355
 QY 373 CGAGCCATGCGCGCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 432
 Db 356 CGAGCCATGCGCGCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 415
 QY 433 AAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 492
 Db 416 AAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 475
 QY 493 CTCTGGCCAGAGCCGGGATATACAGAGGTCGACGCTTAATCGGAATTTCTGGGCG 552
 Db 476 CTCTGGCCAGAGCCGGGATATACAGAGGTCGACGCTTAATCGGAATTTCTGGGCG 535
 QY 553 TAAAGCCGCTAGGTGTTGTTGTTAAGTCGATGGAATCCAGGCTCAACCTTGAA 612
 Db 536 TAAAGCCGCTAGGTGTTGTTGTTAAGTTGATGGAAGCCCGGCTCAACCTTGAA 595
 QY 613 TGGCACCCTACTAGCTAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 672
 Db 596 CTGCATTCAAAACGACAGTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 655
 QY 673 GTGAATGCGTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 732
 Db 656 GTGAATGCGTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 715
 QY 733 TGACACTGAGTGGCGAAGCCGTGGGAGCAACAGGATTAGATACCTGCTGATGCTCAACGCG 792

Db 716 TGACCTAGGTGCGAAGCGTGGGGAGCAACAGATTAGATACCTGTGATGCCAGC 775
QY 793 CGTAAACGATGCTCTAGACCGTTGG--GTTGTATGACTTAGTGGCGAGCTAAAGCAA 850
Db 776 CGTAAACGATGCTCACTGACCGTGGAGCCTTAGCTTTAGTGGCGAGCTAAAGCAA 835
QY 851 TAAAGTAGACCGCTGGGAGATACGCGCGCAAGTTAAACTCAATATATTGACGGGGC 910
Db 836 TAAAGTAGACCGCTGGGAGATACGCGCGCAAGTTAAACTCAATATATTGACGGGGC 895
QY 911 CCGCAACAAGCGGTGGAGCATGTGTTTAATCGAAGCAACGCAAGAACTTACTACTC 970
Db 896 CCGCAACAAGCGGTGGAGCATGTGTTTAATCGAAGCAACGCAAGAACTTACTACTC 955
QY 971 TTGACATCCACAGAACATTTAGAGATCAGATGATGCTGCTGGGAACTGTGAACAGGTG 1030
Db 956 TTGACATCCAAATGAATCTTCCAGAGATGATGGTGGCTTGGGAACTTGAACAGGTG 1015
QY 1031 CTGCATGGCTGCTGACAGCTGCTGTGTGTAATGTGGTTAAGTCCCGTAAGAGGCA 1090
Db 1016 CTGCATGGCTGCTGACAGCTGCTGTGTGTAATGTGGTTAAGTCCCGTAAGAGGCA 1075
QY 1091 ACCCTTGCTCTATTATTTGCGAGCAGCTAATGTTGGGAACTTTAAGAGACTGCGGTGACA 1150
Db 1076 ACCCTTGCTCTATTATTTGCGAGCAGCTAATGTTGGGCACTTTAAGAGACTGCGGTGACA 1135
QY 1151 AACCGGAGAGAGGTGGGAGACAGCTCAATCATATGCGCTTACGATGAGGTACACA 1210
Db 1136 AACCGGAGAGAGGTGGGAGATGACCTCAATCATATGCGCTTACGAGCTGAGCTACACA 1195
QY 1211 CGTGTCACTACATGCGCTATACAGAGGCTGCAAGCTAGAGATAGAGCAAGTCCCAAAA 1270
Db 1196 CGTGTCACTACATGCGCTATACAGAGGCTTCCAGCCGAGGTGAGCTAATCCCAAAA 1255
QY 1271 GTAAGCTGTAATGCGGAGTTGAGTGTGAACTGCACTCATGAAATGGAATGCTAATGTA 1330
Db 1256 ACCGATCGTATGCGGAGTGCAGTGTGCACTGCGTGAATGCGAATGCTAATGTA 1315
QY 1331 ATCGGAATCAGAAATGTCACGCGTGAATGCTCCCGGCGCTTGAACACCGCGCTGAC 1390
Db 1316 ATCGGAATCAGAAATGTCGCGGTGAATGCTCCCGGCGCTTGAACACCGCGCTGAC 1375
QY 1391 ACCATGGAATGTAATGCTCCAGAAATGAGCTTAACCTTGGGGATGCGGTTACC 1450
Db 1376 ACCATGGAATGTAATGCTCCAGAAATGAGCTTAACCTTGGGGATGCGGTTACC 1433
QY 1451 ACCGAGTGTCAATGACTGGGTGAAATCTAC 1483
Db 1434 ACCGAGTGTCAATGACTGGGTGAAATCTAC 1466

RESULT 3

US-09-745-476-1
; Sequence 1, Application US/09745476
; Patent No. 6521429
; GENERAL INFORMATION:
; APPLICANT: CANON INC.
; TITLE OF INVENTION: Preparation of Poly-hydroxyalkanoic Acid
; FILE REFERENCE: 4351008
; CURRENT APPLICATION NUMBER: US/09/745,476
; CURRENT FILING DATE: 2000-12-26
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Microsoft Word
; SEQ ID NO 1
; LENGTH: 1501
; TYPE: DNA
; ORGANISM: Pseudomonas jesseni P161 ; FERM P-17445
US-09-745-476-1

Query Match 76.1%; Score 1131; DB 4; Length 1501;
Best Local Similarity 88.2%; Pred. No. 0;
Matches 1299; Conservative 0; Mismatches 165; Indels 9; Gaps 6;

QY 13 TGAACGCTGCGCAGGCTTTAAACATGCAAGTCAAGCGGTACAGGGAGCTTGCTCC 72
Db 1 TGAACGCTGCGCAGGCTTTAAACATGCAAGTCAAGCGGTACAGGGAGCTTGCTCC 58
QY 73 TGCAGAGAGCGCGGAGCGGGTGAATACCGGTAGAAATGTGCTGATAGAGGGAGCAA 132
Db 59 TGAATTC-AGCGCGGAGCGGGTGAATACCGGTAGAAATGTGCTGATAGAGGGAGCAA 117
QY 133 CATGTGAAAAGCATGTCTAATACCGCATACCGCTTGAAGGGGAAAGAGAGGAGCACTTTCG 192
Db 118 CGTCTCGAAAAGGAGCGCTAATATCCGCAATAGCTCTACGGGAAAGAAACAGGGAG--CCTTC 175
QY 193 GAGCCTTCCGTATTAATATAGCTGCTGTGAATATAGCTAAGTGAAGGTAAAGGCTTA 252
Db 176 GAGCCTTCCGTATTAATATAGCTGCTGTGAATATAGCTAAGTGAAGGTAAAGGCTTA 235
QY 253 CCAAGGCGACGATCTTAATGCTGTGAGAGATGACCAAGTCACTAGGAGTACAGACAC 312
Db 236 CCAAGGCGACGATCTTAATGCTGTGAGAGATGATCAAGTCACTAGGAGTACAGACAC 295
QY 313 GGCCTCAAGCTCTACGAGAGGACAGAGTGGGAAATTTGGAATATGAGGCGCAAGCTTAT 372
Db 296 GATCAGACTCTACGAGAGGACAGAGTGGGAAATTTGGAATATGAGGCGCAAGCTTAT 355
QY 373 CCAAGCAGTCCGCGTGTGAGAGAGCCTTAAGGTTGTAAGCACTTACAGGCGTGAAG 432
Db 356 CCAAGCAGTCCGCGTGTGAGAGAGCCTTACAGGTTGTAAGCACTTACAGGCGTGAAG 415
QY 433 AAGGATGATAGTTAATAGCTTATCATCTTACAGTTAGCCCGCAAGAAAGACCGGCTAA 492
Db 416 AAGGATGATAGTTAATAGCTTATCATCTTACAGTTAGCCCGCAAGAAAGACCGGCTAA 475
QY 493 CTCTGTGCGACGACCGCGGTATATACAGAGGAGGCAAGGTTAATGGAATTAATCTGAGG 552
Db 476 CTCTGTGCGACGACCGCGGTATATACAGAGGAGGCAAGGTTAATGGAATTAATCTGAGG 535
QY 553 TAAAGCGCGCTAGTGTGTTGTAAGTTCGATGTGAATATCCAGGAGCTCAACTTGAA 612
Db 536 TAAAGCGCGCTAGTGTGTTGTAAGTTCGATGTGAATATCCAGGAGCTCAACTTGAA 595
QY 613 TGGCAACCGATACGTGCTAGCTAGATGTGTGAGAGGGGTGTGGATTTTCTGTGTAGG 672
Db 596 CTGATTTCAAACTGCAAGACTAGAGTGTGTGAGAGGGGTGTGGATTTTCTGTGTAGG 655
QY 673 GTGAATATCCGATATATAGGAAGCAATCAGTGGCGAAGCGCACACCTGACTATATAC 732
Db 656 GTGAATATCCGATATATAGGAAGCAATCAGTGGCGAAGCGCACACCTGACTATATAC 715
QY 733 TGAACCTGAGTGGGAAAGCGTGGGAGCAAAAGAAATTAATACCTGTGATGCCAGC 792
Db 716 TGAACCTGAGTGGGAAAGCGTGGGAGCAAAAGAAATTAATACCTGTGATGCCAGC 775
QY 793 CGTAAAGATGTCTACTAGACCGTTGG--GTTGTATGACTTAGTGGCGAGCTTAAGCAA 850
Db 776 CGTAAAGATGTCTACTAGACCGTTGGAGCCTTGAAGCTCTTAGTGGCGAGCTTAAGCAA 835
QY 851 TAAAGTAGACCGCTGGGAGTACGCGCGCAAGTTAAACTCAATATATTGACGGGGC 910
Db 836 TAAAGTAGACCGCTGGGAGTACGCGCGCAAGTTAAACTCAATATATTGACGGGGC 895
QY 911 CCGCAACAAGCGGTGGAGCATGTGTTTAATCGAAGCAACGCAAGAACTTACTACTC 970
Db 896 CCGCAACAAGCGGTGGAGCATGTGTTTAATCGAAGCAACGCAAGAACTTACTACTC 955
QY 971 TTGACATCCACAGAACATTTAGAGATCAGATGATGCTTGGGAACTGTGAACAGGTG 1030
Db 956 TTGACATCCAAATGAATCTTCCAGAGATGATGGTGGCTTGGGAACTTGAACAGGTG 1015
QY 1031 CTGCATGGCTGCTGACAGCTGCTGTGTGTAATGTGGTTAAGTCCCGTAAGAGGCA 1090
Db 1016 CTGCATGGCTGCTGACAGCTGCTGTGTGTAATGTGGTTAAGTCCCGTAAGAGAGGCA 1075
QY 1091 ACCCTTGCTCTATTATTTGCGAGCAGCTAATGTTGGGAACTTTAAGAGACTGCGGTGACA 1150

Db 1076 ACCCTTCTCTTATTACCAAGCAAGTATGTGGGCACTCTTAAGGAGACTTGGCGGTGACA 1135
Oy 1151 AACCGAGAGAGTGGGAGAGAGTCAATCATATGAGCCCTTAAGAGAGGCTTACACA 1210
Db 1136 AACCGAGAGAGTGGGAGAGTCAATCATATGAGCCCTTAAGAGAGGCTTACACA 1195
Oy 1211 CTGTCTCAATATGCGATATACAGAGGCTGCAAGCTAGCAATATGAGAGCAATCCACAA 1270
Db 1196 CTGTCTCAATATGCGATATACAGAGGCTGCAAGCTAGCAATATGAGAGCAATCCACAA 1255
Oy 1271 GTAGTGTGTAGTCCGAGTGGAGTCTGCACTGATCCATTAAGTCCGAATCCGATAGA 1330
Db 1256 ACCGATGTAGTCCGAGTGGAGTCCGAGTGGAGTCCGAGTGGAGTCCGAGTGGAGT 1315
Oy 1331 ATCGTGAATCAGAAATGTCAAGGATACGTTCCCGGCTTGTACACACCCCGCTGAC 1390
Db 1316 ATCGGAAATCAGAAATGTCAAGGATACGTTCCCGGCTTGTACACACCCCGCTGAC 1375
Oy 1391 ACCATGGAGTGTATGCTTCTCAGAGTACGATCTTAACCTTCGGGATGGCGGTTAC 1450
Db 1376 ACCATGGAGTGTATGCTTCTCAGAGTACGATCTTAACCTTCGGGATGGCGGTTAC 1433
Oy 1451 ACGAGTGTATGATCTGAGGCTTGAAGTCTAC 1483
Db 1434 ACGGTGTATGATCTGAGGCTTGAAGTCTAC 1466

RESULT 4

US-09-748-205-1
; Sequence 1, Application US/05748205
; Patent No. 6586562

GENERAL INFORMATION:

; APPLICANT: Canon, Inc.
; TITLE OF INVENTION: Polyhydroxyalkanoate its manufacturing method, and microorganism
; TITLE OF INVENTION: those are used for the method.
; FILE REFERENCE: 4351009
; CURRENT APPLICATION NUMBER: US/09/748,205
; CURRENT FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 1

; SEQ ID NO: 1
; LENGTH: 1501

; TYPE: DNA

; ORGANISM: Pseudomonas jessenii 161 strain.

US-09-748-205-1

Query Match 76.1%; Score 1131; DB 4; Length 1501;
Best Local Similarity 88.2%; Pred. No. 0;

Matches 1299; Conservative 0; Mismatches 165; Indels 9; Gaps 6;

Oy 13 TGAACGCTGCGGAGGCTTAAACATGCAAGTCGAGCGGTAAACAGGAGCTTGTCC 72
Db 1 TGAACGCTGCGGAGGCTTAAACATGCAAGTCGAGCGGTAAACAGGAGCTTGTCC 58
Oy 73 TGCAGAGAGCGGAGCGGTGATGTAACCGGTAGAAATCTGCTAGTGAAGGAGACA 132
Db 59 TGAATTC-AGCGGCGGAGCGGTGATGTAACCGGTAGAAATCTGCTAGTGAAGGAGACA 117
Oy 133 CATGTGAAACGATGATTAATACCGCATACGCTTGAAGGAGGAAAGAGGAGACTTTCG 192
Db 118 CGTCTGAAAGGAGCGCTAATACCGCATACGCTTGAAGGAGGAAAGAGGAGACTTTCG 175
Oy 193 GAGCTTCCGCTAATTAAGTAGAGCTGCTGAGTACTGATGTTGGTAAAGGCTTA 252
Db 176 GAGCTTCCGCTAATTAAGTAGAGCTGCTGAGTACTGATGTTGGTAAAGGCTTA 235
Oy 253 CCAAGGAGAGATCTTAATCTGCTGAGAGATGACAGTCACTAGGAGCTGAGAC 312
Db 236 CCAAGGAGAGATCTTAATCTGCTGAGAGATGATCACTGAGAACTGAGAC 295
Oy 313 GAGCCAGACTCTTAACGAGGAGCAGAGTGGGAAATTTGGAATATGGGCGCAAGCTTAT 372
Db 296 GATCAGACTCTTAACGAGGAGCAGAGTGGGAAATTTGGAATATGGGCGCAAGCTTAT 355

Oy 373 CCAAGCATCCGCTGTGTGAAGAAAGCCTTAAGGTTGTAAGCACTTTCAGGGGTAGG 432
Db 356 CCAAGCATCCGCTGTGTGAAGAAAGCCTTCCGATTTGAAGCACTTTAAGTGGAGG 415
Oy 433 AAGGTGATAGTTAATAGTTATCATCTTGAAGTACCCCAAGAAAGAGACCGGCTTA 492
Db 416 AAGGTGATAGTTAATAGTTATCATCTTGAAGTACCCCAAGAAAGAGACCGGCTTA 475
Oy 493 CTCTGTCCAGAGAGCGCGGTATACAGAGGCTGCAAGCTTAATTCGAATTAAGTGGCG 552
Db 476 CTCTGTCCAGAGAGCGCGGTATACAGAGGCTGCAAGCTTAATTCGAATTAAGTGGCG 535
Oy 553 TAAAGCGCGGTAGTGTGTTTCTTAAGTGTGAATCCAGGCTCAAGCTTGA 612
Db 536 TAAAGCGCGGTAGTGTGTTTCTTAAGTGTGAATCCAGGCTCAAGCTTGA 595
Oy 613 TGGCACCAGTACTGCTAGTATAGTATGAGAGGAGTGGAAATTTCTGTAGCG 672
Db 596 CTGCATTAAGAACTGACAAAGTATGATATGATAGGATGGATTTCTGTAGCG 655
Oy 673 GTGAATGCTGATATAGAAAGAAATCATGATGCGAAGCGACACCTTGACTATAC 732
Db 656 GTGAATGCTGATATAGAAAGAAATCATGATGCGAAGCGACACCTTGACTATAC 715
Oy 733 TGAATGCTGATATAGAAAGAAATCATGATGCGAAGCGACACCTTGACTATAC 792
Db 716 TGAATGCTGATATAGAAAGAAATCATGATGCGAAGCGACACCTTGACTATAC 775
Oy 793 CGTAAACGATGTCTACTAGCGGTGG--GTGTAAATGACTAGTGGCGACATACGAA 850
Db 776 CGTAAACGATGTCTACTAGCGGTGG--GTGTAAATGACTAGTGGCGACATACGAA 835
Oy 851 TAAGTACCGCTGCGGAGTACCGGCGCAAGTAAATCAATGAATTAAGGAGGAG 910
Db 836 TAAGTACCGCTGCGGAGTACCGGCGCAAGTAAATCAATGAATTAAGGAGGAG 895
Oy 911 CCGCAGAGCGGTGAGCATGTGTATTAATGAAAGCAAGCGAAGAACTTACTATC 970
Db 896 CCGCAGAGCGGTGAGCATGTGTATTAATGAAAGCAAGCGAAGAACTTACTATC 955
Oy 971 TTGACATCCAGAAATTTGAGATAGATGTGCTTGGGAACTGTGAGACAGTG 1030
Db 956 TTGACATCCAAATGAATTTCAAGATGATGAGGCTTGGGAACTGTGAGACAGTG 1015
Oy 1031 CTGCATGCTGTGCTAGCTGCTGTGTAATGTTGGTAAATGCTCCGTAAACAGAGCA 1090
Db 1016 CTGCATGCTGTGCTAGCTGCTGTGTAATGTTGGTAAATGCTCCGTAAACAGAGCA 1075
Oy 1091 ACCCTGTCTTATTTGCAAGCATATGCTGGAACTTTAAGGAGACTGCGGTACA 1150
Db 1076 ACCCTGTCTTATTTGCAAGCATATGCTGGAACTTTAAGGAGACTGCGGTACA 1135
Oy 1151 AACCGAGAGAGTGGGAGCGAGTCAAGTCAATGCTAGGCTTGAAGTGGGCTACACA 1210
Db 1136 AACCGAGAGAGTGGGAGCGAGTCAAGTCAATGCTAGGCTTGAAGTGGGCTACACA 1195
Oy 1211 CGTCTACATATGCGGTATACAGAGGCTGCAAGCTTGAAGTGGGCTTGAAGTGGGCT 1270
Db 1196 CGTCTACATATGCTGATACAGAGGCTTGAAGTGGGCTTGAAGTGGGCTTGAAGTGGGCT 1255
Oy 1271 GTACGTGATGCTGAGTGTGATGCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 1330
Db 1256 ACCGATGTAGTCCGATGTGCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 1315
Oy 1331 ATCGTGAATCAGAAATGTCAAGGATACGTTCCCGGCTTGTACACACCCCGCTGAC 1390
Db 1316 ATCGGAAATCAGAAATGTCAAGGATACGTTCCCGGCTTGTACACACCCCGCTGAC 1375
Oy 1391 ACCATGGAGTGTATGCTTCTCAGAGTACGATCTTAACCTTCGGGATGGCGGTTAC 1450
Db 1376 ACCATGGAGTGTATGCTTCTCAGAGTACGATCTTAACCTTCGGGATGGCGGTTAC 1433

QY 1451 ACGAGTGGTCATGACTGGGGTTGAAGTCTAC 1483
 1434 ACGGTGATTCATGACTGGGGTGAAGTCTTAC 1466
 Db

RESULT 5

US-08-114-695A-6
Sequence 6, Application US/08114695A
Patent No. 5508193
GENERAL INFORMATION:
APPLICANT: Mandelbaum, Raphael T.
TITLE OF INVENTION: DEGRADATION OF S-TRIAZINES IN SOIL AND
TITLE OF INVENTION: WATER
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCHWEGMAN, LUNDBERG & WOESSNER, P.A.
STREET: 3500 IDS CENTER
CITY: MINNEAPOLIS
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/114,695A
FILING DATE: 31-AUG-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MUEITING, ANN M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 600.268US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-0331
TELEFAX: 612-339-3061
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1518 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: rRNA
ORIGINAL SOURCE:
ORGANISM: pseudomonas aeruginosa
US-08-114-695A-6

Query Match 74.7%; Score 1109.4; DB 1; Length 1518;
Best Local Similarity 69.0%; Pred. No. 0;
Matches 1023; Conservative 192; Indels 9; Gaps 6;

[illegible]

QY	30	ACTGACACAGCGGCCCAAGACTCTCTACGGGAGCAGCAGTGGGAAATTGTGACAAATGGCG	362
Db	316	ACTGACACAGCGGCCCAAGACTCTCTACGGGAGCAGCAGTGGGAAATTGTGACAAATGGCG	375
QY	363	CAAGCTGATCCAGCATGCGCGTGTGTGAAGAGCGCTTAGGGTTGTAAACACTTTC	422
Db	376	AAAGCCNAGVCCAGCCATGCGCGGTGTGTGAAGAGCGCTTAGGGTTGTAAACACTTTC	435
QY	423	AGGGGTGAGGAGGGGTGATAGGTTAATAGCTTATCATCTTGACGTTAGCCCAAGAGAG	482
Db	436	AGUGGGAGAGGGGCAAGUAAUAAUCCUUCUUGUUGAAGUUAACAAGAUAG	495
QY	483	CACCGGCTAACTCTGTGCACAGACCGCGGTTAATACAGAGGGTGCAGCGTTAATCGAA	542
Db	496	CACCGGCTAACTCTGTGCACAGACCGCGGTTAATACAGAGGGTGCAGCGTTAATCGAA	555
QY	543	TTATCTGAGCGTAAAGCGCGCTAGCTGTGTTAAAGTGGATGTGAATCCCAAGGCTC	602
Db	556	TTATCTGAGCGTAAAGCGCGCTAGCTGTGTTAAAGTGGATGTGAATCCCAAGGCTC	615
QY	603	AACTTGAGATGGCACCAGTACTGCTAGATGATGATGAGAGGGGTGTGGAATTC	662
Db	616	AACTTGAGATGGCACCAGTACTGCTAGATGATGATGAGAGGGGTGTGGAATTC	675
QY	663	CTGTGTAGCGGTAAGTAATCGTATGATATGAAAGAAATCATGATGCGAAAGCGACACT	722
Db	676	CTGTGTAGCGGTAAGTAATCGTATGATATGAAAGAAATCATGATGCGAAAGCGACACT	735
QY	723	GAGCTAATCTGACATGAGGTGGGAAAGGTGGGAGCAAAACAGATTTAGTATCCCTGG	782
Db	736	GAGCTAATCTGACATGAGGTGGGAAAGGTGGGAGCAAAACAGATTTAGTATCCCTGG	795
QY	783	TAGTCCACCCCTTAACCATGTCTACTAGCCGTTGAGTT--GTTAATGACTTATGTCGCA	840
Db	796	UAGUCCAGCCGUAACCAUUGUCACTAGCCGTTGAGTT--GTTAATGACTTATGTCGCA	855
QY	841	GCTAAGCAATTAAGTATGACCGGCTGGGGAATACGCGCGCAAGTTTAACTCAATGAT	900
Db	856	GCTAAGCAATTAAGTATGACCGGCTGGGGAATACGCGCGCAAGTTTAACTCAATGAT	915
QY	901	TGACGGGGGCCCGGCAAGCGGTGAGCATGTGTTTATTCGAAGCAACGGAAGAAC	960
Db	916	UAGCGGGGCCCGGCAAGCGGTGAGCATGTGTTTATTCGAAGCAACGGAAGAAC	975
QY	961	TTAAGCTCTTGTGATCATCACAAGAACTTTGAGAGATCAGATGTGCTCTTGGGAACTGT	1020
Db	976	TTAAGCTCTTGTGATCATCACAAGAACTTTGAGAGATCAGATGTGCTCTTGGGAACTGT	1035
QY	1021	GAGACAGGTGTGATGTGCTGTGTGTGAGTGTGTTGTTGGTTTAAAGTCCGCT	1080
Db	1036	GAGACAGGTGTGATGTGCTGTGTGTGAGTGTGTTGTTGGTTTAAAGTCCGCT	1095
QY	1081	AAAGACCGCAACCTTGTCTTATTTTCCACAGACGTAATGTGTGGAACTTTAAGAGACT	1140
Db	1096	AAAGACCGCAACCTTGTCTTATTTTCCACAGACGTAATGTGTGGAACTTTAAGAGACT	1154
QY	1141	GCGGATGACAAACCGAGAGAGAGTGGGAGAGAGTCAATCAATCATGCGCCTTACAGAT	1200
Db	1155	GCGGATGACAAACCGAGAGAGAGTGGGAGAGAGTCAATCAATCATGCGCCTTACAGAT	1214
QY	1201	GGGCTTACACATGTGTCAATATGTGTATACAGAGGCTCGAAGCTTAGCATATGATAGCA	1260
Db	1215	GGGCTTACACATGTGTCAATATGTGTATACAGAGGCTCGAAGCTTAGCATATGATAGCA	1274
QY	1261	ATCCCAACAAGTACGTGTGTATCCGATTTGGAATCTTGCACTGCACTCAATATAAGTCGA	1320
Db	1275	ATCCCAACAAGTACGTGTGTATCCGATTTGGAATCTTGCACTGCACTCAATATAAGTCGA	1334
QY	1321	ATCGCTAGTAATCGTAATTCAGATTTTCAAGGTGATTAAGTTCGCGGCGCTTGTACAC	1380
Db	1335	ATCGCTAGTAATCGTAATTCAGATTTTCAAGGTGATTAAGTTCGCGGCGCTTGTACAC	1394
QY	1381	CGCGGCTACACATGGAGTTGATTTGCTCAAGATAGTACTTAACTTTCGGGAT	1440

Db 1377 ACACCGCCCTCAACCATGGAGGAGTTGATTCCTCAAGAGTACTTAACCTTTCGG 1436
1396 ACACCGCCCTCAACCATGGAGGAGTTGATTCCTCAAGAGTACTTAACCTTTCGG 1453
Qy 1437 GGATGGGCGTTTACCGAGGAGTGTCAATGACTGGGGT 1473
Db 1454 GGAGGCGCTTACCACTTTGTGATTCATGACTGGGGT 1490

RESULT 7

US-09-465-355-2
; Sequence 2, Application US/09465355
; Patent No. 6316194
; GENERAL INFORMATION:
; APPLICANT: Karm, Jonathan
; APPLICANT: Knowles, David
; APPLICANT: Knowles, Alastair
; APPLICANT: Lentzen, Georg
; TITLE OF INVENTION: Methods and Kits for Discovery of RNA-Binding Antimicrobials
; FILE REFERENCE: 22620/1150 (Formerly 3950/852761)
; CURRENT FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: US 09/325,601
; PRIOR FILING DATE: 1999-06-03
; PRIOR APPLICATION NUMBER: GB 9812196.5
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: GB 9904790.4
; PRIOR FILING DATE: 1999-03-02
; PRIOR APPLICATION NUMBER: US 60/122,439
; PRIOR FILING DATE: 1999-03-02
; PRIOR APPLICATION NUMBER: US 60/088,241
; PRIOR FILING DATE: 1998-06-05
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 1542
; TYPE: RNA
; ORGANISM: Escherichia coli
US-09-465-355-2

Query Match 71.6%; Score 1064.6; DB 4; Length 1542;
Best Local Similarity 68.8%; Pred. No. 0;
Matches 1016; Conservative 250; Mismatches 199; Indels 12; Gaps 7;

Qy 3 TAGCTCAGATTGAAGCGTGGGCGAGGCTTAACACATGCAAGTCCAGCGGTAAACAG-- 60
Db 20 UGCGUCAGAUUGAACGCGGCGGAGGCGU--AACACAUUGCAAGUCGUAACGUAACAGAA 78
Qy 61 GGAAGTGTCTCC--TGCTGACGAGCGGCGGACGCGGTGAGTACGCGGTAGAAATCTGCTTA 118
Db 79 GAAAGCUCUCUCUCUCUGACGAGUGGCGGAGGUAAGUAGUCUGGAAACUGCCUG 138
Qy 119 GTAAGGGGGGACACATGTGGAACGCAATGTAATCCGATACCGCTCGAGGGGGGAAAG 178
Db 139 AUGAGGGGGGUAACUACUGGAACGUGAUCUAUACCGCAUAACGUCGCAAGACCAAG 198
Qy 179 GAGGGGACTCTTCGAGGCTTCGCTATTAGATGAGCTGCGTGAAGATTAGCTAGTTGCT 238
Db 199 AGGGGGA--CCUUGGGGCGUCUCUCCAUUGGAGUGGCCAGUGGGAUUAGCUAGUAGGU 256
Qy 229 AGGTAAGGCTTACCAAGGAGAGATCTTAATCTGCTGAAGAGATGACCAAGTACAC 298
Db 257 GGGGUAACGCGUCACUGAGCGAGGAGCCUAGUGUGUCUGAGAGGUAUGACCAAGCCAC 316
Qy 299 TGGGACTGAGACAGCGGCGCAGACTCTTAACGAGGAGCAGTGGGGAATATTGACATG 358
Db 317 UGGAACUGAGACAGGUCACAGACUACUGGAGGAGCAGUGGGGAUAUUGCAUAUG 376
Qy 359 GCGGAAAGCTGATCCAGGCTATGCCGCGTGTGTGAAGAAAGCCTTAGGCTTGAAGAC 418
Db 377 GCGGAAAGCTGATCCAGGCTATGCCGCGTGTGTGAAGAAAGCCTTAGGCTTGAAGAC 436

Qy 419 TTTCAGGGGTGAGGAAGGTGTATAGTTAATACGTTATCATCTTGACGTTAGCCCCAGAA 478
Db 437 TTTCAGGGGTGAGGAAGGTGTATAGTTAATACGTTATCATCTTGACGTTAGCCCCAGAA 496
Qy 479 GAAGCAACCGCTTAATCTGTGCGACAGCCGCGTAAATACAGAGGGTCAAGCCTTAATC 538
Db 497 GAAGCAACCGCTTAATCTGTGCGACAGCCGCGTAAATACAGAGGGTCAAGCCTTAATC 556
Qy 539 GGAATTACTGGGCGTAAACCGCGCTGAGTGTGTTAATGCTCGGATGTGAATCTCCAG 598
Db 557 GGAATUACUGGGGUAACCGCGCTGAGTGTGTTAATGCTCGGATGTGAATCTCCAG 616
Qy 599 GCTCAACCTTGAATGACCGCATGCTGCTAGTGAATGATGATGAGGAGGCTGTGAA 658
Db 617 GCTCAACCTTGAATGACCGCATGCTGCTAGTGAATGATGATGAGGAGGCTGTGAA 676
Qy 659 TTTCCTGTAGCGGTGAATATGAGTAAATAGAGAAACATCATGTCGAGAGCGACA 718
Db 677 TTTCCTGTAGCGGTGAATATGAGTAAATAGAGAAACATCATGTCGAGAGCGACA 736
Qy 719 CCTGAGCTAATACCTGACCTGAGGCGAAACGCTGGGGGAGCAACGATTAATGATAC 778
Db 737 CCTGAGCTAATACCTGACCTGAGGCGAAACGCTGGGGGAGCAACGATTAATGATAC 796
Qy 779 CTGTAGTCCAGCGCTTAACGATGCTACTAGCCG--TTGGTGTATGACTAGTGG 836
Db 797 CTGTAGTCCAGCGCTTAACGATGCTACTAGCCG--TTGGTGTATGACTAGTGG 856
Qy 837 CGAGCTAATACCTGATGATGACCGCTGGGGAGTACCGCGCAAGCTTAATGATAC 896
Db 857 CGAGCTAATACCTGATGATGACCGCTGGGGAGTACCGCGCAAGCTTAATGATAC 916
Qy 897 GAATTGACGGGGGCGCGCAAGCGGTGAGTGTGTTAATGAGCAACGCGAAG 956
Db 917 GAATTGACGGGGGCGCGCAAGCGGTGAGTGTGTTAATGAGCAACGCGAAG 976
Qy 957 AACCTTACTCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1016
Db 977 AACCTTACTCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATG 1036
Qy 1017 CTGTGAGACAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1076
Db 1037 CTGTGAGACAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1096
Qy 1077 CCGTAACGAGCGCAACCTTGTCTTATTGCGACAGTAAATGTTGGAACTTTAAGAA 1136
Db 1097 CCGTAACGAGCGCAACCTTGTCTTATTGCGACAGTAAATGTTGGAACTTTAAGAA 1156
Qy 1137 GACTGCGGCTGACCAACCGGAGAGTGGGAGCAGACGTCATGATGATGATGATGATG 1196
Db 1156 GACTGCGGCTGACCAACCGGAGAGTGGGAGCAGACGTCATGATGATGATGATGATG 1216
Qy 1197 AGTAGGCTTACACAGCTGCTTACATGCTTATACAGAGGCTGACAGTGAAGTGA 1256
Db 1216 AGTAGGCTTACACAGCTGCTTACATGCTTATACAGAGGCTGACAGTGAAGTGA 1276
Qy 1257 GCGAATCCACCAAGTACCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 1316
Db 1276 GCGAATCCACCAAGTACCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 1336
Qy 1317 CGGAATGCTTGAATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATG 1376
Db 1336 CGGAATGCTTGAATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATG 1396
Qy 1377 ACACCGCGCTGACCAACGAGGAGTGTGCTCCAGAAATGATGATGATGATGATGATG 1436
Db 1396 ACACCGCGCTGACCAACGAGGAGTGTGCTCCAGAAATGATGATGATGATGATGATG 1453
Qy 1437 GGATGGGCTTACCAAGGAGTGTGATGATGATGATGATGATGATGATGATGATGATG 1473
Db 1454 GGATGGGCTTACCAAGGAGTGTGATGATGATGATGATGATGATGATGATGATGATG 1490


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RESULT 9
US-08-114-695A-1
; Sequence 1, Application US/08114695A
; Patent No. 5508193
; GENERAL INFORMATION:
; APPLICANT: Mandelbaum, Raphael T.
; APPLICANT: Mackert, Lawrence P.
; TITLE OF INVENTION: DEGRADATION OF S-TRIAZINES IN SOIL AND
; TITLE OF INVENTION: WATER
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCHWEGMAN, LUNDBERG & MOESSNER, P.A.
; STREET: 3500 IDS CENTER
; CITY: MINNEAPOLIS
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/114,695A
; FILING DATE: 31-AUG-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MOETING, ANN M.
; REGISTRATION NUMBER: 33,977
; REFERENCE/DOCKET NUMBER: 600,268US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-339-0331
; TELEFAX: 612-339-3051
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1542 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: rRNA
; ORIGIN: SOURCE:
; ORGANISM: Escherichia coli
;
US-08-114-695A-1
Query Match 71.3%; Score 1058.8; DB 1; Length 1542;
Best Local Similarity 68.3%; Pred. No. 0;
Matches 1009; Conservative 248; Mismatches 207; Indels 14; Gaps 6;

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QY 358 GGGCGCAAGCCTGATCCAGCCATGCCCGCTGTGTGAAGAAGCCTTAGGTTGTAAGA 417
DB 376 GGGCGCAAGCCTGATCCAGCCATGCCCGCTGTGTGAAGAAGCCTTAGGTTGTAAGA 435
QY 418 CTTTCAGAGGGTGAAGAAGGTTGATGTTAATACGTTATCATCTTGACCTTAGACCCAGA 477
DB 436 CTUUCACGGGGAGGAAGGAGUAAGUAUACCTUUCUACUUAACGUCUACCCGCACA 495
QY 478 AGAAGCACCGGCTTACTCTGTCCAGACAGCCCGGTTAATACAGAGGTTCCAGCTTAAT 537
DB 496 AGAAGCACCGGCTTACTCTGTCCAGACAGCCCGGTTAATACAGAGGTTCCAGCTTAAT 555
QY 538 CGGATTTACTGGGGTAAAGCCGCGTAGGTTGTTAAGCGGATGTGAATCCGAG 597
DB 556 CGGATTTACTGGGGTAAAGCCGCGTAGGTTGTTAAGCGGATGTGAATCCGAG 615
QY 598 GGGTCAACCTTGAAATGGCAACCCGATACGTGCTAGTAGTATGATAGAGGGTGTGA 657
DB 616 GGGTCAACCTTGAAATGGCAACCCGATACGTGCTAGTAGTATGATAGAGGGTGTGA 675
QY 658 ATTTCCTGTAGCGGTGAAGTATGCTATGATATGAAAGAAATCATAGTGGCAAGCGAC 717
DB 676 ATTTCCTGTAGCGGTGAAGTATGCTATGATATGAAAGAAATCATAGTGGCAAGCGAC 735
QY 718 ACCCTGACTAATATCTGACACTGAGGTGCGAAAGCCTGGGAGCAAAACAGATTAGATAC 777
DB 736 ACCCTGACTAATATCTGACACTGAGGTGCGAAAGCCTGGGAGCAAAACAGATTAGATAC 795
QY 778 CTTGTAGTCCAGCGCTTAAAGATGTCTACTAGCCG--TTGGGTTTAAATACCTTAGTG 835
DB 796 CTTGTAGTCCAGCGCTTAAAGATGTCTACTAGCCG--TTGGGTTTAAATACCTTAGTG 855
QY 836 GCGCAGCTTAACGCAATAGTAGACCGCTGTGGGAGTACCGCCAGGTTAAACTCAAA 895
DB 856 GCGCAGCTTAACGCAATAGTAGACCGCTGTGGGAGTACCGCCAGGTTAAACTCAAA 915
QY 896 TGAATTGACGGGGGCCGCAAGCGGTGAGCATGTGTTAATTGAAACGCGAA 955
DB 916 TGAATTGACGGGGGCCGCAAGCGGTGAGCATGTGTTAATTGAAACGCGAA 975
QY 956 GAACCTTACTACTCTTTGATCATCAGAAACATTGAGAGATCAGATGGTCTTCGAGA 1015
DB 976 GAACCTTACTACTCTTTGATCATCAGAAACATTGAGAGATCAGATGGTCTTCGAGA 1035
QY 1016 ACTGTGAGACAGGTGTGTCATGCTGTGTCAGCTGTGTTGAAATGTTGGTTAAT 1075
DB 1036 ACTGTGAGACAGGTGTGTCATGCTGTGTCAGCTGTGTTGAAATGTTGGTTAAT 1095
QY 1076 CCCGTAACGAGCGCAACCTTGTCTTATTGTCGACAGATAGTGGGAACTTTAAG 1135
DB 1096 CCCGTAACGAGCGCAACCTTGTCTTATTGTCGACAGATAGTGGGAACTTTAAG 1154
QY 1136 AGACTCGCGGTGAACAAACCGAGAGAGTGGGAGCAGACTCAAGTCAATCATGACCTTAA 1195
DB 1155 AGACTCGCGGTGAACAAACCGAGAGAGTGGGAGCAGACTCAAGTCAATCATGACCTTAA 1214
QY 1196 GAGTAGGCTTACACAGCTGTCTACATGCGGTATACAGAGGCTGCAAGCTTACGATG 1255
DB 1215 GAGTAGGCTTACACAGCTGTCTACATGCGGTATACAGAGGCTGCAAGCTTACGATG 1274
QY 1256 AGCGAATCCGCAAAAGTAGTGTGTCAGGATGAGTGTGCAACTGCACTCAATGAAG 1315
DB 1275 AGCGAATCCGCAAAAGTAGTGTGTCAGGATGAGTGTGCAACTGCACTCAATGAAG 1334
QY 1316 TCGGAATCGTGTAGTAATCGTGAATCGAAATGTCACGCTGAATACGTTCCCGGCTTGA 1375
DB 1335 TCGGAATCGTGTAGTAATCGTGAATCGAAATGTCACGCTGAATACGTTCCCGGCTTGA 1394
QY 1376 CACACCGCGCGTACACACAGTGGAGTTGTTGTCAGAGTAAAGCTTAAACCTTGG 1435
DB 1395 CACACCGCGCGTACACACAGTGGAGTTGTTGTTGTCAGAGTAAAGCTTAAACCTTGG 1452

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Db 1397 CACGCCGCTCACACCATGGAGATTTGATACAGAGGGGTAGGCTAAC--TTGG 1454
Qy 1438 GATGGCGGTACACGAGTGTGTATGAC 1467
Db 1455 GAGCGCGCTCACACGAGTGTATGATCAGAC 1484

RESULT 11

US-08-299-810A-27
Sequence 27, Application US/08299810A
Patent No. 5721097
GENERAL INFORMATION:
APPLICANT: Rosseau, Rudi
APPLICANT: Van Heuverswyn, Hugo
TITLE OF INVENTION: HYBRIDIZATION PROBES FOR THE
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESS: Merchant & Gould
STREET: 3100 No. 5721097west Center
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/299,810A
FILING DATE: 01-SEP-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hillson, Randall A.
REGISTRATION NUMBER: 31,838
REFERENCE/DOCKET NUMBER: 8076.70-US-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 1485 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Brachymeria catanthalis
IMMEDIATE SOURCE:
CLONE: 16S rRNA Gene
US-08-299-810A-27

Query Match 69.3%; Score 1039; DB 1; Length 1485;
Best Local Similarity 85.3%; Pred. No. 0;
Matches 1332; Conservative 0; Mismatches 196; Indels 16; Gaps 6;

Qy 32 TAAACATGCAAGTCGAGCGGTAAACAGGGAGCTTCTGCTGCTGACGAGCGCGGAGC 91
Db 5 TTAACACATGCAAGTCGAC--GAAGTAGGAAGCTTCTGATCTTAGTGGCGGAG 63
Qy 92 GGTAGTAGCGCGTAGAATCTGCTAGTAGAGGGGAGCAACATGAGAAAGCGATGCTA 151
Db 64 GGTAGTAGCTTAGAATCTGCTAGTAGAGGGGAGTAACTTGGGAAACCAAGCTA 123
Qy 152 ATACCGCATACGCCCTGAGGGGGAAAGAGAGGAGCTTTCGAGCCTTCGCTATTAGT 211
Db 124 ATACCGCATACGACTACGGGTGAAGGGGCTTT-----AGCTTCGCTATTAGT 176
Qy 212 GAGCTGCTGAGATAGCTAGTGTGTAAGGCTTAAAGCCCTACCAAGCGACATCTCTA 271
Db 177 GAGCTTAACTGAGATAGCTAGTGTGTAAGGCTTAAAGCCCTACCAAGCGACATCTCTA 236

Qy 272 CTGCTGAGAGATACCAATCACTGGAATGAGACAGGCCCAAGCTCTTACGGGA 331
Db 237 CTGCTGAGAGATATACGCCACCTGGAGCTAGAGACGGCCCAAGCTCTTACGGGA 296
Qy 332 GAGAGAGTGGGAAATTGACAAATGGGCGAAGCTTATCCAGCATGCGCGTGTGT 391
Db 297 GAGAGAGTGGGAAATTGACAAATGGGCGAAGCTTATCCAGCATGCGCGTGTGT 356
Qy 392 GAAAGAGCTTATGAGTTGTAAGCACTTTCAGGGGTGAGAGAGGTGATAGTATAC 451
Db 357 GAAAGAGCTTATGAGTTGTAAGCACTTTCAGGGGTGAGAGAGGTGATAGTATAC 416
Qy 452 GTATATCATCTGACCTTACGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 511
Db 417 CATTAGCCCTGACCTTACGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 476
Qy 512 GTATACAGAGGGTGCACACCTTATCGGAATTAATGAGCGGTAAAGCGCGTAGTGT 571
Db 477 GTATACAGAGGGTGCACACCTTATCGGAATTAATGAGCGGTAAAGCGCGTAGTGT 535
Qy 572 TTGTTAGTCGATGAGTGAATCCAGGGGCTCAACCTTGGATGACCCGATCTGGCTA 631
Db 536 TATTAGTGAATGTAAGAGCCCGGCTTAACTCGGAGTGCATCTGATCTGATA 595
Qy 632 GCTAGAGTATGATAGAGGGGTGGAATTTCTGTGTAGCGGTGAATGCGTATATAG 691
Db 596 ACTAGAGTATGATAGAGGGGTGGAATTTCTGTGTAGCGGTGAATGCGTATATAG 655
Qy 692 GAAAGAACTCAATGCGGAGAGGAGACCTTGAATTAATCTGACACTGAGGTGGAA 751
Db 656 GAAAGAACTCAATGCGGAGAGGAGACCTTGAATTAATCTGACACTGAGGTGGAA 715
Qy 752 CGTGGGAGCAACAGATTAATGATACCTGTAGTCCAGCGGTAAAGATGCTACTAG 811
Db 716 CGTGGGAGCAACAGATTAATGATACCTGTAGTCCAGCGGTAAAGATGCTACTAG 775
Qy 812 CCGTTGGG--TTGTAATGATTAATGAGCGGAGCTTAAAGCGGTAAAGATGCTACTAG 869
Db 776 TCGTTGGGCTTTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCT 835
Qy 870 GTACGCGCGCAAGTAAATCAATTAATGATGAGCGGGGCGCGACAGCGGTGAGCA 929
Db 836 GTACGCGCGCAAGTAAATCAATTAATGATGAGCGGGGCGCGACAGCGGTGAGCA 895
Qy 930 TGTGTTTAAATTGAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 989
Db 896 TGTGTTTAAATTGAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 955
Qy 990 TGAGAGTCAAGTGTGCTTGGGAGACTGTGAGCAGGTGCTGATGGCTGTGCTACG 1049
Db 956 GCAAGAGTCAAGTGTGCTTGGGAGACTGTGAGCAGGTGCTGATGGCTGTGCTACG 1015
Qy 1050 TCGTGTGTAATGATGAGTGTGAGTAAAGTCCGCTAGAGAGCGCAAGCCCTGCTATTTC 1109
Db 1016 TCGTGTGTAATGATGAGTGTGAGTAAAGTCCGCTAGAGAGCGCAAGCCCTGCTATTTC 1075
Qy 1110 AGCAGCTAATGATGAGTGTGAGTAAAGTCCGCTAGAGAGCGCAAGCCCTGCTATTTC 1169
Db 1076 AGCAGCTAATGATGAGTGTGAGTAAAGTCCGCTAGAGAGCGCAAGCCCTGCTATTTC 1134
Qy 1170 GCAAGTCAATGATGAGTGTGAGTAAAGTCCGCTAGAGAGCGCAAGCCCTGCTATTTC 1229
Db 1135 GCAAGTCAATGATGAGTGTGAGTAAAGTCCGCTAGAGAGCGCAAGCCCTGCTATTTC 1194
Qy 1230 CAGAGGCTGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1289
Db 1195 CAGAGGCTGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1254
Qy 1290 GAGTGTGCAACTGACCTCATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1349
Db 1255 GAGTGTGCAACTGACCTCATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1314
Qy 1350 CGGTGAATACGTTCCGGGCTTTGTAACACCGCCCGTACACATGGAGTTGATGCT 1405

Db 1315 CGGTGATAGCTTCCCGGGCCCTTGTACACACCGCCCTGCACACCATGGAGTTATCTCA 1374
QY 1410 CCAGAGTAGTACTAGCTTACCTTGGGGGATGGCGGTACACGAGAGTGCATGACTG 1469
Db 1375 CCAGAGTGGTATGCTTACGCG---AGAGGGCGATCACCGGTGGGTGATGACTG 1430
QY 1470 GGGT 1473
Db 1431 GGGT 1434

RESULT 12
US-09-228-184-1
; Sequence 1, Application US/09228184
; Patent No. 6322782
; GENERAL INFORMATION:
; APPLICANT: WALKER, Harrell L.
; APPLICANT: HIGGINBOTHAM, Lawrence R.
; TITLE OF INVENTION: CONTROL OF CYANOBACTERIA WITH A BACTERIUM
; FILE REFERENCE: 013243-0007
; CURRENT APPLICATION NUMBER: US/09/228,184
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1540
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURES:
; OTHER INFORMATION: Description of Unknown Organism: Bacterium SG-3;
; OTHER INFORMATION: gram negative; rod-shaped; exhibits flagellae;
; OTHER INFORMATION: motility; pathogenic to cyanobacteria and algae;
; OTHER INFORMATION: yellow colonies on BG-11 medium suppl. with tryptic
US-09-228-184-1

Query Match 69.2%; Score 1028.2; DB 4; Length 1540;
Best Local Similarity 83.7%; Pred. No. 0;
Matches 1238; Conservative 0; Mismatches 228; Indels 13; Gaps 6;

QY 3 TACCTGAGTGAACGCTGCGGCGGCTTAAACATGACAGTGCAGCGGTACAGGG 62
Db 16 TGGCTGAGGTGACCGCTGCGGCGGCTTAAACATGACAGTGCAGCGGTACAGGG 74
QY 63 AGCT---TGCTCTGCTGACGAGCGGCGGCTGAGTAAAGGCTGAGTCTGCTA 118
Db 75 AGTAGCAATAGTGTGGGTGGCGAGTGGCGGACGGTGAAGAAATCATCGAATGCCCCA 134
QY 119 GTAGAGGGGCAACATGTGGAACGATGCTAATACCGCATACGCTTGAAGGGAAG 178
Db 135 GTGCTGGGGATTAACATAGGAACTTATGCTAATACCGCATACGCTTGAAGGGAAG 194
QY 179 GAGGGAGCTTCTCGAGCCTTCCGCTATTAGATGAGCTGCGTGAAGTAACTAGTTGT 238
Db 195 CGGGGA--TCGGAACCTCGCGCATTTGATGAGCCGATGTCGATTAAGTTGCG 252
QY 239 AGGGTAAAGGCTTACCAAGGCGAAGATCTTAACTGTGTGAGAGATGACCAAGTCAAC 298
Db 253 GGGGTATGCGCCACCAAGGCGAAGATCGGTGCTGTGAGAGATGACCAAGTCAAC 312
QY 299 TGGAGCTGAGACAGCGCCAGACTCTTACGAGAGGAGAGGAGGAGTATTTGACATG 358
Db 313 TGAAGCTGAGACAGCGTCCAGACTCTTACGAGAGGAGAGGAGGAGTATTTGACATG 372
QY 359 GCGGCAAGCTGTATCCAGCATGCGGTGTGTGAAGAGGCTTAAAGGCTTGAAGAC 418
Db 373 GCGGCAAGCTGTATCCAGCATGCGGTGTGTGAAGAGGCTTAAAGGCTTGAAGAC 432
QY 419 TTTCAGGGGTGAGAGAGGAGTATGATGATATCATCTTGAAGTCCCGCAAG 478
Db 433 TTTTGTCCGAAAGAAAGACATGATTAATCTTGTGCTGATGATGATGATGATGATGAT 492
QY 479 GAAGCAAGGCTTACTCTGTGTCCAGAGCGCGGTATATCAAGAGGTGCAAGCTTATCT 538

Db 493 TAAGACCGGCTAATCTTGTGTCAGAGCGCGGCTAATAGAGGGGTGCAAGGTTACTC 552
QY 539 GGAATTACTGGGCGTAAAGCGCGGTAGGTGTTTGTATGATGGATGTAAATCCAGG 598
Db 553 GGAATTACTGGGCGTAAAGCGGTAGGTGTTTGTATGATGGATGTAAATCCAGG 612
QY 599 GCTCAAGCTTGAATGGCAACCGATGCTGATGATGATGATGATGATGATGATGATG 658
Db 613 GCTCAAGCTTGAATGGCAACCGATGCTGATGATGATGATGATGATGATGATGATG 672
QY 659 TTTCCTGTAGCGGTGAAATGCTGATATTAAGAGGAAATCAATGAGGAGGAGGAGCA 718
Db 673 TTCCGGGTAGCAAGTAAATGCTGATGATGATGATGATGATGATGATGATGATG 732
QY 719 CCTGAGTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 778
Db 723 ATCTGAGCAAGCACTGACATGAGGCAAGAAAGGTGGGAGCAACAGATTAGATCC 792
QY 779 CTGATAGTCCAGCGCGTAAAGATGATGATGATGATGATGATGATGATGATGATG 835
Db 793 CTGATAGTCCAGCGCGTAAAGATGATGATGATGATGATGATGATGATGATGATG 852
QY 836 GCGCAGCTAAGCAATAGTAAAGCGCGGTGAGTACGCGCGCAAGGTTAAACTCAAA 895
Db 853 TCGAAGCTAAGCGCTTAAAGTTCGCGCGTGGGAGTACGCTCCCAAGACTGAACCTCAA 912
QY 896 TGAATGAGCGGGCGCGCAAGCGGTGAGTACGCTGATGATGATGATGATGATGATG 955
Db 913 GGAATGAGCGGGCGCGCAAGCGGTGAGTACGCTGATGATGATGATGATGATGATG 972
QY 956 GAACCTTACTACTCTTGAATGATGATGATGATGATGATGATGATGATGATGATG 1015
Db 973 GAACCTTACTACTCTTGAATGATGATGATGATGATGATGATGATGATGATGATG 1032
QY 1016 ACTGTGAGACAGGTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 1075
Db 1033 ACCGTGAGACAGGTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 1092
QY 1076 CCGTAAAGAGCGCAACCGTGTCTTATTTGACAGCACTAATGAGGAACTTAAAG 1135
Db 1093 CCGGAGAGAGCGCAACCGTGTCTTATTTGACAGCACTAATGAGGAACTTAAAG 1152
QY 1136 AGACTGCGGTGACAAACCGGAGAGGTGGGACGAGTCAATGATCAATGAGGCTTAC 1195
Db 1153 AGACTGCGGTGACAAACCGGAGAGGTGGGACGAGTCAATGATCAATGAGGCTTAC 1212
QY 1196 GAGTGGGCTTACACCGTGTCAATGAGGAGTGGGAGTGGGAGTGGGAGTGGGAG 1255
Db 1213 GGCAGGGCTTACACCGTGTCAATGAGGAGTGGGAGTGGGAGTGGGAGTGGGAG 1272
QY 1256 AGCGAATCCCAAAAGTACGTGTAGTCCGATGAGTGGGAGTGGGAGTGGGAGTGG 1315
Db 1273 AGCGAATCCCAAAAGTACGTGTAGTCCGATGAGTGGGAGTGGGAGTGGGAGTGG 1332
QY 1316 TCGAATGCTAGTATGATGATGATGATGATGATGATGATGATGATGATGATG 1374
Db 1333 TCGAATGCTAGTATGATGATGATGATGATGATGATGATGATGATGATGATG 1392
QY 1375 ACACACCGCGCTGACACATGAGGAGTGAATGCTCCAGAGTGAAGTGAAGTGAAG 1434
Db 1393 ACACACCGCGCTGACACATGAGGAGTGAATGCTCCAGAGTGAAGTGAAGTGAAG 1452
QY 1435 GGGGATGGCGGTACAGAGAGTGTCAATGATGAGTGGGT 1473
Db 1453 GGGG--GGCGCTTGCACAGTGTGCGAGTACGAGGT 1489

RESULT 13
US-09-967-376-1
; Sequence 1, Application US/09967376
; Patent No. 6482635
; GENERAL INFORMATION:

APPLICANT: WALKER, Harrell L.
 APPLICANT: HIGGINBOTHAM, Lawrence R.
 TITLE OF INVENTION: CONTROL OF CYANOBACTERIA WITH A BACTERIUM
 FILE REFERENCE: 013243-0007
 CURRENT APPLICATION NUMBER: US/09/967,376
 CURRENT FILING DATE: 2001-09-28
 NUMBER OF SEQ ID NOS: 1
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 1
 LENGTH: 1540
 TYPE: DNA
 ORGANISM: Unknown Organism
 FEATURE:
 OTHER INFORMATION: Description of Unknown Organism: Bacterium SG-3; gram negative;
 OTHER INFORMATION: rod-shaped; exhibits flagellate motility; pathogenic to
 OTHER INFORMATION: cyanobacteria and algae; yellow colonies on BG-11 medium suppl.
 US-09-967-376-1

Query Match 69.2%; Score 1028.2; DB 4; Length 1540;
 Best Local Similarity 83.7%; Pred. No. 0;
 Matches 1238; Conservative 0; Mismatches 228; Indels 13; Gaps 6;

QY 3 TAGCTCAATGGAACGCTGCGCAGGCTTAAACATGCAAGTCGACGGCTAACAGGGG 62
 DB 16 TGGCTCAGAGTGAACGCTGCGCAGGCTTAAACATGCAAGTCGACGGCTAACAG 74
 QY 63 AGCT---TGCTCCGTGCTGAGAGGCGGCGGCTGATGTAAGCGGATGAGATCTGCT 118
 DB 75 ATGACCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 134
 QY 119 GTAGAGGGGGAACAATGCTGGAACGATGCTAATACCGATACCGCTTGAAGGGGGA 178
 DB 135 GTCTGGGGGGAATACATAGGAACTTATGCTAATACCGATACCGCTTGAAGGGG 194
 QY 179 GAGGGGACTCTTCCGAGCTTCCGCTATTAATAGAGCTGCGGATTAAGTAACTTGT 238
 DB 195 CGGGGGA--TCGCAAGACTTCCGCTGATGATGATGATGATGATGATGATGATG 252
 QY 239 AGGTAAAGGCTTACCAAGGCGAGATCTTAACTGCTGAGAGTACAGCACTGACAC 298
 DB 253 GGGGTAATGCGCCACCAAGGCGAGATGATGATGATGATGATGATGATGATGATG 312
 QY 299 TGGAGCTAGACAGGCGCCAGATCTTACGAGAGGCGAGCTGGGATTTTGAACATG 358
 DB 313 TGGAACTAGACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 372
 QY 359 GCGGAGGCTGATCAGCACTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 418
 DB 373 GCGGAGGCTGATCAGCACTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 432
 QY 419 TTTCAGGGGTAGAGAGGGGTATAGTTAATCGTTATCATCTTGACCTTACCCGAGA 478
 DB 433 TTTCAGGGGTAGAGAGGGGTATAGTTAATCGTTATCATCTTGACCTTACCCGAGA 492
 QY 479 GAAGAGCGGGCTAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 538
 DB 493 TAAAGACCGGCTAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 552
 QY 539 GGAATTAATGCGCTTAAAGCGCGCTAGTGTGTTTGAAGTGGATGTAATCCGAG 598
 DB 553 GGAATTAATGCGCTTAAAGCGCGCTAGTGTGTTTGAAGTGGATGTAATCCGAG 612
 QY 599 GGTCAACTTGAATGGAACCGGCTAGTGTGTTTGAAGTGGATGTAATCCGAG 658
 DB 613 GGTCAACTTGAATGGAACCGGCTAGTGTGTTTGAAGTGGATGTAATCCGAG 672
 QY 659 TTTCCTGTAGCGGTGAATGCTGATATAGAGAGGATCATCAGTGGAGAGCGAGAC 718
 DB 673 TTCCCGGTGTAGCGGTGAATGCTGATATAGAGAGGATCATCAGTGGAGAGCGAG 732
 QY 719 CCTGAGCTAATATCTGACATGAGGTGCGAAGCTGGGAGCGAAGAGATTAATGATC 778

DB 733 ATTCGACGACGACTGACACTGAGGACGAGAAAGCTGGGAGGAGAAACAGATTAGATCC 792
 QY 779 CTGTGATGCAAGCGCGTAAACGATGCTCTACAGCCGTGGGT---TGATATGACTTAGT 835
 DB 793 CTGTGATGCAAGCGCGTAAACGATGCTCTACAGCCGTGGGT---TGATATGACTTAGT 852
 QY 836 GCGGAGCTAAGCAATAGTGAAGCGCGCTGGGAGTACCGCGCAAGGTTAAACCTCAA 895
 DB 853 TCGAAGCTAAGCAATAGTGAAGCGCGCTGGGAGTACCGCGCAAGGTTAAACCTCAA 912
 QY 896 TGAATGACGCGGCGCGCGCAAGCGGTGAGCATGTGTTTAAATTCGAGCAAGCGGA 955
 DB 913 GGAATGACGCGGCGCGCGCAAGCGGTGAGCATGTGTTTAAATTCGAGCAAGCGGA 972
 QY 956 GAACCTTACCTGCTTGAATGACAGAGCAATGATGAGATGATGATGATGATGATGAT 1015
 DB 973 GAACCTTACCTGCTTGAATGACAGAGCAATGATGAGATGATGATGATGATGATGAT 1032
 QY 1016 ACTGTGAGACAGGTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1075
 DB 1033 ACGGTGACAGAGGTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1092
 QY 1076 CCGGTACAGAGCGCAACCTTGTCTTATTTGCGAGCACTAATGCTGGAACCTTAAG 1135
 DB 1093 CCGGTACAGAGCGCAACCTTGTCTTATTTGCGAGCACTAATGCTGGAACCTTAAG 1152
 QY 1136 AGACTGCGGTGACCAACCGGAGAGGTGGGAGCAGCTCAAGTCAATGATGCGCTTAC 1195
 DB 1153 AGACGCGCGGAGCAAGCGGAGAGGTGGGAGTACCTCAAGTCAATGATGCGCTTAC 1212
 QY 1196 GAGTAGGCTTACACAGCTGCTAATGCGGTATACAGAGGCTGCAAGCTTACGATAG 1255
 DB 1213 GGCAGAGGCTTACACAGCTTACATGATGCGGAGCAGAGGCTGCAAGCTTACGATAG 1272
 QY 1256 AGCAATCCCAAGAGTGTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 1315
 DB 1273 AGCAATCCCAAGAGTGTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 1332
 QY 1316 TCGAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1374
 DB 1333 TCGAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1392
 QY 1375 ACAACGCGCGGTACACAGTGGAGTGAATGCTGCAAGAGTGAATGATGATGATG 1434
 DB 1393 ACAACGCGCGGTACACAGTGGAGTGAATGCTGCAAGAGTGAATGATGATGATG 1452
 QY 1435 GGGATGCGGTTACCAAGAGTGTCAATGACTGGGCT 1473
 DB 1453 GGGG--GGGCTGCGCAGGTGTGCGGATGACTGGGCT 1489

RESULT 14
 US-09-557-884-1
 Sequence 1, Application US/09557884
 Patent No. 650581
 GENERAL INFORMATION:
 APPLICANT: Fleischmann et al.
 TITLE OF INVENTION: The Nucleotide sequence of
 the Haemophilus influenzae Rd Genome, Fragments
 thereof, and Uses Thereof
 NUMBER OF SEQUENCES: 1
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Human Genome Sciences, Inc.
 STREET: 9410 Key West Avenue
 CITY: Rockville
 STATE: MD
 COUNTRY: USA
 ZIP: 20850
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3 1/2 inch diskette
 COMPUTER: Dell Pentium
 OPERATING SYSTEM: MS DOS v6.22
 SOFTWARE: ASCII Text

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 30, 2004, 19:07:51, Search time 564.517 Seconds
(without alignments)
9593.704 Million cell updates/sec

Title: US-09-737-297-1

Perfect score: 1486

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Scoring table:

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Searched: 2434939 seqs, 1822278265 residues

Total number of hits satisfying chosen parameters: 4869878

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Published Applications NA:
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18: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1486	100.0	1486	9	US-09-737-297-1 Sequence 4, Appli
2	1251.8	84.2	1481	9	US-09-737-297-4 Sequence 1, Appli
3	1131	76.1	1501	9	US-09-791-592-1 Sequence 1, Appli
4	1131	76.1	1501	9	US-09-745-476-1 Sequence 1, Appli
5	1131	76.1	1501	9	US-09-821-016-5 Sequence 5, Appli
6	1131	76.1	1501	9	US-09-748-205-1 Sequence 1, Appli
7	1131	76.1	1501	9	US-09-792-920A-1 Sequence 1, Appli
8	1131	76.1	1501	10	US-09-951-720-1 Sequence 1, Appli
9	1131	76.1	1501	10	US-09-791-610-1 Sequence 1, Appli
10	1131	76.1	1501	13	US-10-242-696-1 Sequence 1, Appli
11	1131	76.1	1501	13	US-10-411-319-1 Sequence 1, Appli
12	1131	76.1	1501	15	US-10-218-519-5 Sequence 5, Appli
13	1131	76.1	1501	15	US-10-266-787-5 Sequence 5, Appli
14	1131	76.1	1501	15	US-10-252-518-5 Sequence 5, Appli
15	1131	76.1	1501	15	US-10-105-305-1 Sequence 1, Appli

16	1131	76.1	1501	15	US-10-133-406A-1 Sequence 1, Appli
17	1114.8	75.0	1424	15	US-10-007-527A-12 Sequence 12, Appli
18	1114.8	75.0	1424	15	US-10-007-452-12 Sequence 12, Appli
19	1113	74.9	1506	13	US-10-278-942-1 Sequence 1, Appli
20	1100.2	74.0	1467	9	US-09-726-774-3 Sequence 3, Appli
21	1071	72.1	1467	13	US-10-029-397A-47 Sequence 47, Appli
22	1068	71.9	1497	14	US-10-007-725-5 Sequence 5, Appli
23	1067.2	71.8	1487	9	US-09-726-774-14 Sequence 14, Appli
24	1065.6	71.7	1541	9	US-09-027-439-7 Sequence 7, Appli
25	1065.4	71.6	1500	9	US-09-726-774-4 Sequence 4, Appli
26	1064.6	71.6	1542	11	US-09-940-925A-158 Sequence 158, App
27	1064.6	71.6	1542	11	US-09-941-193A-158 Sequence 158, App
28	1064.6	71.6	1542	15	US-10-061-071-33 Sequence 33, Appli
29	1059.8	71.3	1506	9	US-09-027-439-3 Sequence 3, Appli
30	1054.4	71.0	1429	10	US-09-934-868-81 Sequence 81, Appli
31	1053.6	70.9	1549	9	US-09-912-020-89 Sequence 89, Appli
32	1053.6	70.9	1549	9	US-09-912-020-242 Sequence 242, App
33	1053.6	70.9	1549	9	US-09-912-020-402 Sequence 402, App
34	1051.4	70.8	1537	13	US-10-029-397A-46 Sequence 46, Appli
35	1051.2	70.7	1485	13	US-10-029-397A-48 Sequence 48, Appli
36	1051.2	70.7	1541	9	US-09-726-774-2 Sequence 2, Appli
37	1049.4	70.6	1505	9	US-09-027-439-4 Sequence 4, Appli
38	1046	70.4	1534	13	US-10-029-397A-35 Sequence 35, Appli
39	1042.6	70.2	1505	9	US-09-027-439-6 Sequence 6, Appli
40	1034	69.6	1450	1	US-09-726-774-1 Sequence 1, Appli
41	1032.8	69.5	1532	14	US-10-007-725-6 Sequence 6, Appli
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43	1028.2	69.2	1540	10	US-09-967-376-1 Sequence 1, Appli
44	1028.2	69.2	1540	10	US-10-260-647-1 Sequence 1, Appli
45	1025.8	69.0	1547	12	US-10-418-861B-53 Sequence 53, Appli

ALIGNMENTS

RESULT 1
US-09-737-297-1
Sequence 1, Application US/09737297
Patent No. US20020072108A1
GENERAL INFORMATION:
APPLICANT: Berry, Mark
APPLICANT: Griffiths, Allen
APPLICANT: Hill, Philip
APPLICANT: Laybourne-Parry, Johanna
TITLE OF INVENTION: Processes and Organisms for the Production of Antifreeze Protein
FILE REFERENCE: F3247
CURRENT APPLICATION NUMBER: US/09/737,297
CURRENT FILING DATE: 2000-12-15
PRIOR APPLICATION NUMBER: GB 9929696.4
PRIOR FILING DATE: 1999-12-15
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 1486
TYPE: DNA
ORGANISM: Marinomonas protea
US-09-737-297-1

Query Match 100.0%; Score 1486; DB 9; Length 1486;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1486; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 GTTGCCTCAATGAAAGCGGCGGAGGCTTAACATGCAAGTCGACGGTAACAG 60
QY 61 GGAAGCTTCTCTGCTGACGAGCGGCGGAGGCTTAACATGCAAGTCGACCTACT 120
DB 61 GGAAGCTTCTCTGCTGACGAGCGGCGGAGGCTTAACATGCAAGTCGACCTACT 120
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Qy 361 CGCAAGCTTATCCAGCCTGCGCTGTGTGAAGAAGGCTTAGCGTTGTAAGCACTT 420
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Qy 421 TCAGGGGTGAGAAAGGTGATAGTTAATACCTTATCACTTGAAGCCCAAGAA 480
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Qy 1321 ATCCGCTAGTAATCGGATCAGAAATGTCAGGATGATACGTTCCCGGAGCTTGTACAC 1380
Db 1321 ATCCGCTAGTAATCGGATCAGAAATGTCAGGATGATACGTTCCCGGAGCTTGTACAC 1380
Qy 1381 CCCCCGTACACATGAGGAGTTGATGCTCCAGAAATGACTTAACTTCCGGGAT 1440
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Qy 1441 GGGGTTACACAGAGTGTGATGATGAGTGGGTTGAAGTCTACGCG 1486
Db 1441 GGGGTTACACAGAGTGTGATGATGAGTGGGTTGAAGTCTACGCG 1486

RESULT 2
US-09-737-297-4
; Sequence 4: Application US/09737297
; Patent No. US20020072108A1
; GENERAL INFORMATION:
; APPLICANT: Beryl, Mark
; APPLICANT: Griffiths, Allen
; APPLICANT: Hill, Philip
; APPLICANT: Laybourne-Parry, Johanna
; APPLICANT: Mills, Sarah
; TITLE OF INVENTION: Processes and Organisms for the Production of Antifreeze Prote
; FILE REFERENCE: F3247
; CURRENT APPLICATION NUMBER: US/09/737,297
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: GB 9929696.4
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 1481
; TYPE: DNA
; ORGANISM: Marinomonas communis
; FEATURE:
; NAME/KEY: Unsure
; LOCATION: (1)..(1)
; OTHER INFORMATION: base identity unsure
; NAME/KEY: Unsure
; LOCATION: (203)..(204)
; OTHER INFORMATION: base identity unsure
; NAME/KEY: Unsure
; LOCATION: (840)..(840)
; OTHER INFORMATION: base identity unsure
; NAME/KEY: Unsure
; LOCATION: (964)..(965)
; OTHER INFORMATION: base identity unsure
; NAME/KEY: Unsure
; LOCATION: (1142)..(1142)
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; NAME/KEY: Unsure
; LOCATION: (1182)..(1182)
; OTHER INFORMATION: base identity unsure
; NAME/KEY: Unsure
; LOCATION: (1185)..(1186)
; OTHER INFORMATION: base identity unsure
; NAME/KEY: Unsure
; LOCATION: (1449)..(1449)
; OTHER INFORMATION: base identity unsure

US-09-737-297-4
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Best Local Similarity 93.7%; Pred. No. 0;
Matches 1374; Conservative 1; Mismatches 83; Indels 9; Gaps 7;

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QY 241 GGTAAAGGCTTCCAAAGGCGAGCATCTCTAACTGATGAGAGGATGACCAAGTCAACTG 300
Db 258 GGTAAAGGCTTCCAAAGGCGAGCATCTCTAGCTGTCTGAGAGATATATACCAACTG 317
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QY 421 TCAGGGGTGAGAGAGGATGATAGTTAATACGTTATCATCTTGAAGTCCGAGAGGA 480
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Db 738 CTGACCGATATCTGACGCTGAGAGTGCAGAAAGCTGGGGAGCGAAACAGGATTAATACCTT 797
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Db 798 GGTAGTCCACCGCGGTAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 857
QY 840 AGCTTAACGCAATAGTATGACCGCTGGGGAGTACGCGCGCAAGGTTAAATCTCAATGAA 899
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QY 900 TTGACGGGGGCGGCGCAAGCGGTGAGCAATGATGATGATGATGATGATGATGATGATGATG 959
Db 918 TTGACGGGGGCGGCGCAAGCGGTGAGCAATGATGATGATGATGATGATGATGATGATGATG 977
QY 960 CTTAACCTACTTGTGACATGACAGAACTTTAGAGATCAGATGATGATGATGATGATGATGATG 1019
Db 978 CTTAACCTACTTGTGACATGACAGAACTTTAGAGATGATGATGATGATGATGATGATGATG 1037
QY 1020 TGAAGACAGTGTCTGACAGTGTGTCTGACGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1079
Db 1038 TGAAGACAGTGTCTGACAGTGTGTCTGACGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1097
QY 1080 TAAACGAGCAACCGCTGTCTTATTTGACAGCACTAATGATGATGATGATGATGATGATGATG 1139
Db 1098 TAAACGAGCAACCGCTGTCTTATTTGACAGCACTAATGATGATGATGATGATGATGATGATG 1156

QY 1140 TGGCGGTGACAAACCGGAGAGAGTGGGGAGCAAGTCAAGTCAATGAGCCCTTACAGAT 1199
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QY 1200 AGGGCTACACAGCTGTCTTCAATGAGCGGTATACAGAGGCGCTGCAAGCTAAGATGAGCG 1259
Db 1217 AGGGCTACACAGCTGTCTTCAATGAGCGGTATACAGAGGCGCGCAAGCTGCGAGGATGAGCA 1276
QY 1260 AATCCACAAAGTACGTCGATAGTCCGATGAGTGTGCAACTGCACTCAGTCAATGAGTGG 1319
Db 1277 AATCCACAAAGTACGTCGATAGTCCGATGAGTGTGCAACTGCACTCAGTCAATGAGTGG 1336
QY 1320 AATCGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1379
Db 1337 AATCGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1396
QY 1380 CCGCGCGTACACAGCTGAGTGTGATGCTGCGAAGTACGATGATGATGATGATGATGATGATG 1439
Db 1397 CCGCGCGTACACAGCTGAGTGTGATGCTGCGAAGTACGATGATGATGATGATGATGATGATG 1454
QY 1440 TGGCGGTACACAGGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1466
Db 1455 TGGCGGTACACAGGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1481

RESULT 3
US-09-791-592-1
; Sequence 1, Application US/09791592
; Patent No. US20010021223A1
; GENERAL INFORMATION:
; APPLICANT: Canon Inc.
; TITLE OF INVENTION: Polyhydroxyalkanoate containing 3-hydroxybenzoate
; FILE REFERENCE: 4396021
; CURRENT APPLICATION NUMBER: US/09/791,592
; CURRENT FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 1
; SEQ ID NO 1
; LENGTH: 1501
; TYPE: DNA
; ORGANISM: Pseudomonas jessenii 161 strain.
US-09-791-592-1

Query Match 76.1%; Score 1131; DB 9; Length 1501;
Best Local Similarity 88.2%; Pred. No. 1e-298; Indels 9; Gaps 6;
Matches 1299; Conservative 0; Mismatches 165;

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1 TGAACGCTGGCGGAGGCGCTTAAACATGACATGACGCGGTAAACAGGGAGCTTGTCTCC 58
QY 73 TGTGACGAGGCGGCGGAGGCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 132
Db 59 TGAATTC-AGGCGGAGGCGGAGGCGGTGATGATGATGATGATGATGATGATGATGATGATGATG 117
QY 133 CATGAGAAAGCATGCTAATATACCGCATACGCGCTGAGGGGAAAGAGGGGACTTCTCG 192
Db 118 CGTCTGAAAGGAGCGCTAATATACCGCATACGCGCTGAGGGGAAAGAGGGGACTTCTCG 175
QY 193 GAGCCTTCGCTAATGATGAGCTGCGTGAATGATGATGATGATGATGATGATGATGATGATGATG 252
Db 176 GGGCGCTTCGCTAATGATGAGCTGCGTGAATGATGATGATGATGATGATGATGATGATGATGATG 235
QY 253 CCAAGGCGAGATGCTAATACGCGCTGAGAGATGACCACTGACACTGAGGAGTGAAGAC 312
Db 236 CCAAGGCGAGATGCTAATACGCGCTGAGAGATGACCACTGACACTGAGGAGTGAAGAC 295
QY 313 GCGCCGAGCTCTTACGCGGAGGAGCAAGTGGGAAATATTGACCAATGAGGCGCAAGCTGAT 372
Db 236 GGTCCAGACTCTTACGCGGAGGAGCAAGTGGGAAATATTGACCAATGAGGCGCAAGCTGAT 355
QY 373 CCAAGCAGTCCGCGTGTGTGAAGAGGCTTAAAGGCTTAAAGCACTTAAAGGAGTGAAG 432

DB 356 CCAAGCATGCGCGTGTGAAAGAGCTTGGATTGTAAGCACTTAAAGCTTGGAGG 415
QY 433 AAGGTGATAGGTTAATACGTTATCATCTTGACGTTAGCCCCAGAGAGCAACCGGCTAA 492
DB 416 AAGGGATTAACTTAATACGTTAGTGTGTTGACGTTACCGACAGATTAAGACCGGCTAA 475
QY 493 CTCTGTGACAGACCGCGGCTAATACAGAGGGTGAAGCGTTAATCGGAATTAATGAGGCG 552
DB 476 CTCTGTGACAGACCGCGGCTAATACAGAGGGTGAAGCGTTAATCGGAATTAATGAGGCG 535
QY 553 TAAAGCGCGGTAGGTGTTGTGTTAGTGGATGTAATCCAGGGCTCAACCTTGA 612
DB 536 TAAAGCGCGGTAGGTGTTGTGTTAGTGGATGTAATCCAGGGCTCAACCTTGA 595
QY 613 TGGCACCAGATAGTGGCTAGTAGAGTAGTGAAGGGGTGGAAATTCCTGTGTGCG 672
DB 596 CTGCAATCAAAATGCAAGCTAGAGTAGTAGAGGTGGATGTTCTGTGTGAGCG 655
QY 673 GTGAATGCGTAGATATAGAAAGAAACATCAGTGGCGAAGCGCACCCCTGACTAATAC 732
DB 656 GTGAATGCGTAGATATAGAAAGAAACATCAGTGGCGAAGCGCACCCCTGACTAATAC 715
QY 733 TGACACTGAGGTGCGAAAGCGTGGGAGCAACAGGATTAGTACCTGTGATGCC 792
DB 716 TGACACTGAGGTGCGAAAGCGTGGGAGCAACAGGATTAGTACCTGTGATGCC 775
QY 793 CGTAAAGATGTCTACTAGCCGTTGG--GTGTAATGACTTATGCGCGACCTAAGCA 850
DB 776 CGTAAAGATGTCTACTAGCCGTTGGAGCCTTGAGCTTATGAGGCGACCTAAGCA 835
QY 851 TAAGTAGACCGCTGGGAGATACGCGCGCAAGGTTAAACTCAATGAATTGACGGGCG 910
DB 836 TAAGTAGACCGCTGGGAGATACGCGCGCAAGGTTAAACTCAATGAATTGACGGGCG 895
QY 911 CCGCACAAGCGGTGAGCATGTGTTAATGGAAGCAACGGAAGACCTTACTACTC 970
DB 896 CCGCACAAGCGGTGAGCATGTGTTAATGGAAGCAACGGAAGACCTTACTACTC 955
QY 971 TTGACATCCACAGACATTTAGAGATGATGTGCTTCGGGAATGTGAGACAGGTG 1030
DB 956 TTGACATCCACAGACATTTCAAGATGATGTGCTTCGGGAATGTGAGACAGGTG 1015
QY 1031 CTGATGAGCTGTGTGACGCTGTGTGTAATGTTGGTTAAGTCCGTTACAGAGGCA 1090
DB 1016 CTGATGAGCTGTGTGACGCTGTGTGTAATGTTGGTTAAGTCCGTTACAGAGGCA 1075
QY 1091 ACCCTGTCTTATTGGCAGACGTAATGTGAGAACTTAAAGAGACTCCGGTAGCA 1150
DB 1076 ACCCTGTCTTATTGGCAGACGTAATGTGAGAACTTAAAGAGACTCCGGTAGCA 1135
QY 1151 AACCGAGAGAGGTGGGAGACGTCAGTCAATGATGCTTACGAGTAGGGCTACACA 1210
DB 1136 AACCGAGAGAGGTGGGAGATGACGTCAATGATGCTTACGAGTAGGGCTTACACA 1195
QY 1211 CGTGCTAATGAGCGATACAGAGGCTCAAGCTAAGAGTAGAGCAATCCACAAA 1270
DB 1196 CGTGCTAATGAGCGATACAGAGGCTCAAGCTAAGAGTAGAGCAATCCACAAA 1255
QY 1271 GTAAGTGTAGTCCGATTTGAGACTGTCAACTGACTCCATGAAGTCCGAATCCGTAGTA 1330
DB 1256 ACGGATCGTAGTCCGATTCGCACTGCAACTGCACTGCGTAATCCGAATCCGTAGTA 1315
QY 1331 ATGCTGAATCAGAAATGTCACGAGTAGATGTTCCGGGGCTGTGTACACACCGCGGTAC 1390
DB 1316 ATGCTGAATCAGAAATGTCACGAGTAGATGTTCCGGGGCTGTGTACACACCGCGGTAC 1375
QY 1391 ACCATGGAGATTGATGCTCCAGAAATGACTAATACCTTCGGGGATGGCGTTAC 1450
DB 1376 ACCATGGAGATTGATGCTCCAGAAATGACTAATACCTTCGGGGATGGCGTTAC 1433
QY 1451 ACGGATGCTCAATGACTGGGGTTGAAGCTTAC 1483

DB 1434 ACGGTGATTCATGACTGGGGTGAAGTCGTAC 1466
RESULT 4
US-09-745-476-1
Sequence 1, Application US/09745476
Patent No. US20010029039A1
GENERAL INFORMATION:
APPLICANT: CANON INC.
TITLE OF INVENTION: Preparation of Poly-hydroxylalkanoic Acid
FILE REFERENCE: 435108
CURRENT FILING DATE: 2000-12-26
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Microsoft Word
SEQ ID NO. 1
LENGTH: 1501
TYPE: DNA
ORGANISM: Pseudomonas jessenii P161 ; FERM P-17445
US-09-745-476-1
Query Match 76.1%; Score 1131; DB 9; Length 1501;
Best Local Similarity 88.2%; Pred. No. 1e-298;
Matches 1299; Conservative 0; Mismatches 165; Indels 9; Gaps 6;
QY 13 TGAAGCTGGCGGAGGCTTAAACATGCAATGCAAGCGGTACAGGGAGCTTGCTC 72
DB 1 TGAAGCTGGCGGAGGCTTAAACATGCAATGCAAGCGGTACAGGGAGCTTGCTC 58
QY 73 TGCTACAGAGGCGGAGGCGGTAGTAAAGCGGTAGCAATCGCTAGTAGAGGGAGCAA 132
DB 59 TGAATTC-AGCGGCGAGCGGTAGTAAAGCGGTAGTAAAGCGGTAGTAGAGGGAGCAA 117
QY 133 CATGTGAAAGCAATGCTAATACCGCATACGCGCTGAGGGGAAAGAGGAGGAGCTTTG 192
DB 118 GCTTCGAAGGAGCGGTAAATACCGCATACGCTTACGGAGAAAGAGGAGGAG--CCTTC 175
QY 139 GAGCTTCGCTATTAATGAGCTGCGTGAATTAATGAGTAAAGGCTTAAGGCTTA 252
DB 176 GGGCTTCGCTATTAATGAGCTGCGTGAATTAATGAGTAAAGGCTTAAGGCTTA 235
QY 253 CCAAGGACAGATCTCTAATGCTGAGAGATGACCACTGAGGAGTGAACAC 312
DB 236 CCAAGGACAGATCTCTAATGCTGAGAGATGACCACTGAGGAGTGAACAC 295
QY 313 GCGCCAGATCTCTAATGCGGAGCAAGATGCGGAAATTTGACAAATGAGGCGCAACCTGAT 372
DB 296 GGTTCAGATCTCTAATGCGGAGCAAGATGCGGAAATTTGACAAATGAGGCGCAACCTGAT 355
QY 373 CCAAGCAGTCCGCGTGTGTAAGAGGCTTAAAGGCTTAAAGGCTTAAAGGCTTAAAGG 432
DB 356 CCAAGCAGTCCGCGTGTGTAAGAGGCTTAAAGGCTTAAAGGCTTAAAGGCTTAAAGG 415
QY 433 AAGGTGATAGTAAATGCTTAAATGCTTAAAGGCTTAAAGGCTTAAAGGCTTAAAGG 492
DB 416 AAGGTGATAGTAAATGCTTAAATGCTTAAAGGCTTAAAGGCTTAAAGGCTTAAAGG 475
QY 493 CTCTGTGACAGACCGCGGCTAATACAGAGGGTGAAGCGTTAATCGGAATTAATGAGGCG 552
DB 476 CTCTGTGACAGACCGCGGCTAATACAGAGGGTGAAGCGTTAATCGGAATTAATGAGGCG 535
QY 553 TAAAGCGCGGTAGGTGTTGTGTTAGTGGATGTAATCCAGGGCTCAACCTTGA 612
DB 536 TAAAGCGCGGTAGGTGTTGTGTTAGTGGATGTAATCCAGGGCTCAACCTTGA 595
QY 613 TGGCACCAGATAGTGGCTAGTAGAGTAGTGAAGGGGTGGAAATTCCTGTGTGCG 672
DB 596 CTGCAATCAAAATGCAAGCTAGAGTAGTAGAGGTGGATGTTCTGTGTGAGCG 655
QY 673 GTGAATGCGTAGATATAGAAAGAAACATCAGTGGCGAAGCGCACCCCTGACTAATAC 732
DB 656 GTGAATGCGTAGATATAGAAAGAAACATCAGTGGCGAAGCGCACCCCTGACTAATAC 715

PRIOR FILING DATE: 2000-09-14
 2000-12-13
 2001-05-31
 2001-05-31
 2001-09-11
 NUMBER OF SEQ ID NOS: 1
 SEQ ID NO: 1
 LENGTH: 1501
 TYPE: DNA
 ORGANISM: Pseudomonas jessenii 161 strain.
 US-09-951-720-1

Query Match 76.1%; Score 1131; DB 10; Length 1501;
 Best Local Similarity 88.2%; Pred. No. 1e-298;
 Matches 1299; Conservative 0; Mismatches 165; Indels 9; Gaps 6;

QY 13 TGAACGCTGGCGGAGGCTTAAACACATGCAAGTCAAGCGGTAACAGGGAGCTTCTCC 72
 DB 1 TGAACGCTGGCGGAGGCTTAAACACATGCAAGTCAAGCGGTAACAGGGAGCTTCTCC 58
 QY 73 TGTGACGAGCGGCGAGCGGAGTGAATACGCTAGAGATCTGCTAGTGAAGGAGCA 132
 DB 59 TGAATTC-AGCGCGGAGCGGAGTGAATACGCTAGAGATCTGCTAGTGAAGGAGCA 117
 QY 133 CATGTGAAACGATGCTAAATACCGCATACGCTGAGGGGAGAGAGGAGCTTCTCG 192
 DB 118 CGTCTCGAAAGGAGCGCTAAATACCGCATACGCTGAGGGGAGAGAGGAGCTTCTCG 175
 QY 193 GAGCTTCCGCTATTAATAGCTGCTGAGTGAATAGTGAATGAGTGAAGGAGCTTCTCG 252
 DB 176 GAGCTTCCGCTATTAATAGCTGAGTGAATAGTGAATGAGTGAAGGAGCTTCTCG 235
 QY 253 CCAAGCGAGCGATCTTAATGCTGCTGAGAGATGAACAATGCACTGAGGAGTGAAC 312
 DB 236 CCAAGCGAGCGATCTTAATGCTGCTGAGAGATGAACAATGCACTGAGGAGTGAAC 295
 QY 313 GCGCCAGACTCTTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 372
 DB 296 GGTCCAGACTCTTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 355
 QY 373 CCAGCCATGCGCGCTGTGTGAGAGAGGCTTGAAGGAGGAGGAGGAGGAGGAGGAG 432
 DB 356 CCAGCCATGCGCGCTGTGTGAGAGAGGCTTGAAGGAGGAGGAGGAGGAGGAGGAG 415
 QY 433 AAGGCTATGAGTGAATACGTTATCATCTTGAAGGAGGAGGAGGAGGAGGAGGAG 492
 DB 416 AAGGCTATGAGTGAATACGTTATCATCTTGAAGGAGGAGGAGGAGGAGGAGGAG 475
 QY 493 CTCTGTGCGAGCGCGGAGTGAATACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 552
 DB 476 CTCTGTGCGAGCGCGGAGTGAATACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 535
 QY 553 TAAAGCGCGGAGTGAATGTTTGAAGTGAATGTTTGAAGTGAATGTTTGAAGTGA 612
 DB 536 TAAAGCGCGGAGTGAATGTTTGAAGTGAATGTTTGAAGTGAATGTTTGAAGTGA 595
 QY 613 TGGACCCGAGTACGCTAGTGAATGTTTGAAGTGAATGTTTGAAGTGAATGTTTGA 672
 DB 596 CTGATTTAAAGCTGACAGCTAGTGAATGTTTGAAGTGAATGTTTGAAGTGAATGTT 655
 QY 673 GTGAATGCTAGATATAGAGAGAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 732
 DB 656 GTGAATGCTAGATATAGAGAGAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 715
 QY 733 TGAACCTAGAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 792
 DB 716 TGAACCTAGAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 775
 QY 793 CGTAAACGATGCTACTAGCGCTGG--GTTGATATAGTGAAGGAGGAGGAGGAGGAG 850
 DB 776 CGTAAACGATGCTACTAGCGCTGG--GTTGATATAGTGAAGGAGGAGGAGGAGGAG 835
 QY 851 TGAATTC-AGCGCGGAGCGGAGTGAATGAGGAGGAGGAGGAGGAGGAGGAGGAG 910

DB 836 TAAGTGAACGCGCTGGGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 895
 QY 911 CCGCACAACGCGTGGAGCATGTGTTTAAATGGAAGCAACCGGAGAACTTACTACTC 970
 DB 896 CCGCACAACGCGTGGAGCATGTGTTTAAATGGAAGCAACCGGAGAACTTACTACTC 955
 QY 971 TTGACATCAAGAAACATTTGAGAGATGAGATGAGTGGCTTGGGAGACTGAGAGGAG 1030
 DB 956 TTGACATCAAGAAACATTTGAGAGATGAGATGAGTGGCTTGGGAGAACTTGAAGAG 1015
 QY 1031 CTGATGCTGTGTGTCAGCTGCTGTTGAAATGTTGGTTTAACTCCGTAACAGCGCA 1090
 DB 1016 CTGATGCTGTGTGTCAGCTGCTGTTGAAATGTTGGTTTAACTCCGTAACAGCGCA 1075
 QY 1091 ACCCTGTCTTATTTGCGAGAGCGTAATGAGGAGAACTTAAAGAGCTGCGGAGTGA 1150
 DB 1076 ACCCTGTCTTATTTGCGAGAGCGTAATGAGGAGAACTTAAAGAGCTGCGGAGTGA 1135
 QY 1151 AACCGAGAGAGTGGGAGCGAGCATCAAGTCAATGAGGAGGAGGAGGAGGAGGAG 1210
 DB 1136 AACCGAGAGAGTGGGAGCGAGCATCAAGTCAATGAGGAGGAGGAGGAGGAGGAG 1195
 QY 1211 CGTCTTAATGAGCGATTAAGAGGCTGCAAGTCAAGTCAATGAGGAGGAGGAGGAG 1270
 DB 1196 CGTCTTAATGAGCGATTAAGAGGCTGCAAGTCAAGTCAATGAGGAGGAGGAGGAG 1255
 QY 1271 GTAGTGTGATGCGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 1330
 DB 1256 ACCGATGATAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 1315
 QY 1331 ATGCTGAATGAGTGAATGAGTGAATGAGTGAATGAGTGAATGAGTGAATGAGTGA 1390
 DB 1316 ATGCTGAATGAGTGAATGAGTGAATGAGTGAATGAGTGAATGAGTGAATGAGTGA 1375
 QY 1391 ACCATGAGAGTGAATGAGTGAATGAGTGAATGAGTGAATGAGTGAATGAGTGA 1450
 DB 1376 ACCATGAGAGTGAATGAGTGAATGAGTGAATGAGTGAATGAGTGAATGAGTGA 1433
 QY 1451 ACCGAGTGTCAATGAGTGAATGAGTGAATGAGTGAATGAGTGAATGAGTGA 1483
 DB 1434 ACCGAGTGTCAATGAGTGAATGAGTGAATGAGTGAATGAGTGAATGAGTGA 1466

RESULT 9
 US-09-791-610-1
 Sequence 1, Application US/09791610
 Publication No. US20030100084A1
 GENERAL INFORMATION:
 APPLICANT: Canon Inc.
 TITLE OF INVENTION: Polyhydroxyalkanoate containing 3-hydroxybenzoylalkanoic acid
 FILE REFERENCE: 4396021
 CURRENT APPLICATION NUMBER: US/09/791,610
 CURRENT FILING DATE: 2002-09-30
 NUMBER OF SEQ ID NOS: 1
 SEQ ID NO: 1
 LENGTH: 1501
 TYPE: DNA
 ORGANISM: Pseudomonas jessenii 161 strain.
 US-09-791-610-1

Query Match 76.1%; Score 1131; DB 11; Length 1501;
 Best Local Similarity 88.2%; Pred. No. 1e-298;
 Matches 1299; Conservative 0; Mismatches 165; Indels 9; Gaps 6;

QY 13 TGAACGCTGGCGGAGGCTTAAACACATGCAAGTCAAGCGGTAACAGGGAGCTTCTCC 72
 DB 1 TGAACGCTGGCGGAGGCTTAAACACATGCAAGTCAAGCGGTAACAGGGAGCTTCTCC 58
 QY 73 TGTGACGAGCGGCGAGCGGAGTGAATACGCTAGAGATCTGCTAGTGAAGGAGCA 132
 DB 59 TGAATTC-AGCGCGGAGCGGAGTGAATACGCTAGAGATCTGCTAGTGAAGGAGCA 117


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QY 1271 GNAAGCTGATCCGGAATTGGAGCTGCAACTGCACTCCATGAAGTCGGAATCGGTACTA 1330
Db 1256 ACCGATCGTAGTCCGGATCGCAGCTTCGCACTGACTGCGTGAAGTCGGAATCGGTACTA 1315
QY 1331 ATCGTAATCGAAATGTCACGGTGAATACGTTCCCGGGCCCTTGATACACCGCCCGGTAC 1390
Db 1316 ATCGGAATCGAAATGTCGCGGTGAATACGTTCCCGGGCCCTTGATACACCGCCCGGTAC 1375
QY 1391 ACCATGGAGATGTAATGTCGTCACGAAGTAGTACTTAACCCCTTCGGGGATGCGGTACC 1450
Db 1376 ACCATGGAGATGCGGTTGCAACGAAGTAGTACTTAAC--TTGGGAGAGACGGTTAC 1433
QY 1451 ACGAGTGTCAATGACTGGGGTTGAAGTTCAC 1483
Db 1434 ACGGTGTATCATGACTGGGGTGAAGTCTAC 1466

RESULT 11
US-10-411-319-1
; Sequence 1, Application US/10411319
; Publication No. US20030208029A1
; GENERAL INFORMATION:
; APPLICANT: Canon Inc.
; TITLE OF INVENTION: Polyhydroxamate, Method For Production Thereof And Microorganism
; TITLE OF INVENTION: In The Same
; FILE REFERENCE: 03500.015001.1
; CURRENT APPLICATION NUMBER: US/10/411.319
; PRIOR FILING DATE: 2003-04-11
; PRIORITY APPLICATION NUMBER: US 09/748,205
; PRIOR FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1.1
; SEQ ID NO: 1
; LENGTH: 1501
; TYPE: DNA
; ORGANISM: Pseudomonas jessenii 161 strain
US-10-411-319-1

Query Match 76.1%; Score 1131; DB 13; Length 1501;
Best Local Similarity 88.2%; Pred. No. 1e-295;
Matches 1299; Conservative 0; Mismatches 165; Indels 9; Gaps 6;

QY 13 TGAACGCTGGCGGAGCGCTTAACACATGCAAGTCGAGCGGTACAGCGGAGCTTGCTCC 72
Db 1 TGAACGCTGGCGGAGCGCTT-AACACATGCAAGTCGAGCGG-ATGACGGGAGCTTGCTCC 58
QY 73 TGTGTACGAGCGGCGGAGCGGAGTGAACGGGTGAGAAATGCTGCTGTAGAGGGGACAA 132
Db 59 TGAATTC-AGCGGCGGAGCGGAGTGAATGCTGTGAGAAATGCTGCTGTAGAGGGGACAA 117
QY 133 CATGTGAACCGCATGCTTAATACCGCATACGCTCGAGGGGAAAGAGGGGACTTTGG 192
Db 118 CGTCTGGAAGGAGCGCTAATACCGCATACCTCTTACGGGAGAAAGAGGGGAA--CCTTC 175
QY 193 GACCTTCGCGTATTAGATGAGCGCTGCGGTGAGATTACTGTAGTGTAGAGGTAAGGCTTA 252
Db 176 GGGGCTTCGCGTATGAGATGAGCTTAGTCCGATTACCTAGTGTGAGGTAATGCTCA 235
QY 253 CCAAGGCGACGATCTCTAATCTGCTCGAGAGATGACCAATGCACTGCGACTGAACAC 312
Db 236 CCAAGGCGACGATCCGTAACTGTGTGAGAGATGATCAATGCACTGGAATCGAGACAC 295
QY 313 GGGCCGACATCTTAAGGAGGAGAGAGAGTGGGAATTTGGACATGAGGCGCAAGCTGTAT 372
Db 296 GGTCCAGACTCTTAAGGAGGAGGAGAGTGGGAATTTGGACATGAGGCGCAAGCTGTAT 355
QY 373 CCAAGCATGCGCGTGTGTGAAGAAAGGCTTAGGGTTGAAGCACTTTAGGGGTGAGG 432
Db 356 CCAAGCATGCGCGTGTGTGAAGAAAGGCTTCGAGATGTGAAGCACTTTAGGTGGAGG 415
QY 433 AAGGTGATAGGTAAATACGTTATCATTGAAGTTAGCCCAAGAAACACCGGTTAA 492

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RESULT 11
US-10-411-319-1
; Sequence 1, Application US/10411319
; Publication No. US20030208029A1
GENERAL INFORMATION:
APPLICANT: Canon Inc.
TITLE OF INVENTION: Polyhydroxyrate, Method For Production Thereof And Microorganism
; TITLE OF INVENTION: In the Same
FILE REFERENCE: 03500.015001.1
CURRENT APPLICATION NUMBER: US/10/411,319
CURRENT FILING DATE: 2003-04-11
PRIOR APPLICATION NUMBER: US 09/748,205
PRIOR FILING DATE: 2000-12-27
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn version 3.1
SEQ ID NO. 1
LENGTH: 1501
TYPE: DNA
ORGANISM: Pseudomonas jesseni 161 strain
US-10-411-319-1

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416 AAGGCACTTAACCTAATACGTTAGGTTTGAAGCTTACCGACAGAAATTAAGCAGCGCTAA 475
493 CTCTGTCCAGACACCGCGGTAATACAGAGGGTCCAGCGTTATCGGAATTCCTGGGG 552
476 CTCTGTCCAGACACCGCGGTAATACAGAGGGTCCAGCGTTATCGGAATTCCTGGGG 535
553 TAAAGCGCGGTAGGTGTTGTTAAGTCGGATGTGAATCCGAGGCTCAACCTTGGAA 612
536 TAAAGCGCGGTAGGTGTTGTTAAGTCGGATGTGAATCCGAGGCTCAACCTTGGAA 595
613 TGGACCCCGATCTGGCTAGCTAGATGTGTAGAGGGGTGTGAATTTCTGTGTAGCG 672
536 CTGCATCTAAAACCTACCAAGCTAGAGTATGTAGAGGGGTGTGAATTTCTGTGTAGCG 655
673 GTGAATGCGTATGATATATAGAGAAATCATCAGTGGCGAAGCGCACCTGAGCTAATAC 732
656 GTGAATGCGTATGATATATAGAGAAATCATCAGTGGCGAAGCGCACCTGAGCTAATAC 715
733 TGACACTGAGGTGCGAAGCGTGGGAGCAAAACAGATTAGATACCTGTGTAGTCCAGC 792
716 TGACACTGAGGTGCGAAGCGTGGGAGCAAAACAGATTAGATACCTGTGTAGTCCAGC 775
793 CGTAACGATGCTCTACTGACCGCTGG - GTGTATATGACTTATAGTGGCGAGCTTAAGCAA 850
776 CGTAACGATGCTCTACTGACCGCTGGAGCCTTATAGTGTAGTGGCGAGCTTAAGCAA 835
851 TAAGTAGACCGCGCTGGAGTACGCGCCAGAGTTAAACTCAATGATTTGAAGCGGGCG 910
836 TAAGTAGACCGCGCTGGAGTACGCGCCAGAGTTAAACTCAATGATTTGAAGCGGGCG 895
911 CCGCAAAAGCGGTGAGATGTGTTTAAATTCGAAAGCAAGCGAAAGCTTACCTACTC 970
896 CCGCAAAAGCGGTGAGATGTGTTTAAATTCGAAAGCAAGCGAAAGCTTACCTACTC 955
971 TTGACATCCACAGAACTTTGAGAGATCAGATGGGCTTGGGAGCTGTGAGACAGGTG 1030
956 TTGACATCCACAGAACTTTGAGAGATCAGATGGGCTTGGGAGCTGTGAGACAGGTG 1015
1031 CTGCAATGCTGTCTGACGCTGTGTGAAATGTTGGGTTAAGTCCCGTAACGAGCGCA 1090
1016 CTGCAATGCTGTCTGACGCTGTGTGAAATGTTGGGTTAAGTCCCGTAACGAGCGCA 1075
1091 ACCCTTGTCTTATTTGGCAGACGATATGTTGGGAACTTTAAGAGACCTGCGGGTAC 1150
1076 ACCCTTGTCTTATTTGGCAGACGATATGTTGGGAACTTTAAGAGACCTGCGGGTAC 1135
1151 AACCGAGAGAGTGGGAGCAAGCTCAAGTATCATGAGCTTACGAGTGGGCTACACA 1210
1136 AACCGAGAGAGTGGGAGTACAGTCAAGTATCATGAGCTTACGAGCTTACGAGCTAC 1195
1211 CGTGTACATAGGCTATACAGAGGGCTGCAAGCTAGAGTATGAGCGGAATCCCAAAA 1270
1196 CGTGTACATAGGCTATACAGAGGGTGGCAAGCGCGAGTGGAGCTAATCCCAAAA 1255
1271 GTACGTCGATGCTGGAGTGGAGTCTGCACTGCACTCATGAAGTGGAGTGGAGT 1330
1256 ACCGATGCTGATCCGAGTCGAGCTGCACTGCACTCATGAAGTGGAGTGGAGT 1315
1331 ATCTGATACAGAAATGTCAAGGTGAATACTTCCGGGCTTGTACACACCGCGCTAC 1390
1316 ATCTGATACAGAAATGTCAAGGTGAATACTTCCGGGCTTGTACACACCGCGCTAC 1375
1391 ACCATGGAGTGGATGCTCCAGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGT 1450
1376 ACCATGGAGTGGATGCTCCAGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGT 1433
1451 ACGGAGTGGTCAATGACTGGGGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGT 1483
1434 ACGGAGTGGTCAATGACTGGGGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGT 1466

RESULT 12
US-10-218-519-5

Sequence 5, Application US/10218519
Publication No. US2003049806A1
GENERAL INFORMATION:
APPLICANT: Yano, Tetsuya
APPLICANT: Imamura, Takeshi
APPLICANT: Suda, Sakae
APPLICANT: Homma, Tsutomu
TITLE OF INVENTION: Polyhydroxyalkanoate Synthase and Gene Encoding the Same Enzyme
FILE REFERENCE: 03500.015225.1
CURRENT APPLICATION NUMBER: US/10/218,519
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/821,016
PRIOR FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Microsoft Word
SEQ ID NO 5
LENGTH: 1501
TYPE: DNA
ORGANISM: Pseudomonas jessenii Pl61 ; BP-7376
FEATURE:
FEATURE: cDNA to 16S rRNA
US-10-218-519-5
Query Match 76.1%; Score 1131; DB 15; Length 1501;
Best Local Similarity 88.2%; Pred. No. 1e-298;
Matches 1299; Conservative 0; Mismatches 165; Indels 9; Gaps 6;
13 TGAAGCTGGCGGAGGCTTAAACATGCAATGCGAGGTAACAGGGAGCTTGCTCC 72
1 TGAAGCTGGCGGAGGCTTAAACATGCAATGCGAGGTAACAGGGAGCTTGCTCC 58
73 TGTGACGAGCGCGGAGCGGAGTGAACCGGTGAGATTCGCTGATGAGGGGAGCA 132
59 TGAATTC-AGCGGCGGAGCGGAGTGAATGCTTGAAGATCTGCTGTGTGGGAGCA 117
133 CATGAGGAACGATGCTAATTAACCGCATACCGCTGAGGAGGAGGAGGAGGAGCTTTCG 192
118 GGTCTGAAAGGAGCGCTAATACCGCATGCTGCTACGAGGAGGAGGAGGAGGAGGAG 175
193 GAGCTTCCGCTATTAAGATGAGCGCTGAGATTAAGCTTGAAGTGGAGGAGGAGGAG 252
176 GGGCTTGGCTATCAGATGAGCTGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGT 235
253 CCAAGCGAGAGATCTTAATGCTGCTGAGAGGAGTGAACGCTCACTGAGGAGTGAAGAC 312
236 CCAAGCGAGAGATCTTAATGCTGCTGAGAGGAGTGAACGCTCACTGAGGAGTGAAGAC 295
313 GGGCGAGACTCTACGAGGAGGAGCAAGTGGGAAATTTGACATAGGCGCAAGCTGAT 372
296 GGTCAAGACTCTACGAGGAGGAGCAAGTGGGAAATTTGACATAGGCGCAAGCTGAT 355
373 CCAAGCGAGAGATCTTAATGCTGCTGAGAGGAGTGAACGCTTCAAGGAGTGAAGAG 432
356 CCAAGCGAGAGATCTTAATGCTGCTGAGAGGAGTGAACGCTTCAAGGAGTGAAGAG 415
433 AAGGCTGATGATTAATACGTTATCATCTTGAAGTGGAGGAGGAGGAGGAGGAGGAG 492
416 AAGGCTGATTAATACGTTATGATGTTTGAAGTGAACGAGGAGGAGGAGGAGGAGGAG 475
493 CTCTGTGCGAGACCGCGGATTAACAGAGGAGTGAACGCTTATGGAATTCCTGGGG 552
476 CTCTGTGCGAGACCGCGGATTAACAGAGGAGTGAACGCTTATGGAATTCCTGGGG 535
553 TAAAGCGCGGTAGGTGTTGTTAAGTCGGATGTGAATCCGAGGCTCAACCTTGGAA 612
536 TAAAGCGCGGTAGGTGTTGTTAAGTCGGATGTGAATCCGAGGCTCAACCTTGGAA 595
613 TGGACCCCGATCTGGCTAGCTAGATGTGTAGAGGGGTGTGAATTTCTGTGTAGCG 672
596 CTGCATCTAAAACCTACCAAGCTAGAGTATGTAGAGGGGTGTGAATTTCTGTGTAGCG 655
673 GTGAATGCGTATGATATATAGAGAAATCATCAGTGGCGAAGCGCACCTGAGCTAATAC 732

Dh	656	GTGAATAGCGTATATATAGAAAGGAACACCAAGTGGCGAAAGCGAACCACTGGACTGTATAC	715
Qy	733	TGACACTAGAGGTGCGAAGAAAGCTGGGGAGCAAAACAGATTTAGTATCCTCTGTATGTCACAGC	792
Dh	716	TGACACTGAGGGCGAAGAACCGTGGGAGCAAAACAGATTAGTACCTCTGTATGTCACAGC	775
Qy	793	CGTAAACGATGTCCTACTAGCCGTTGG--GTTGTATATGACTTATGTGGCGCAGCTAACGAA	850
Dh	776	CGTAAACGATGTCCTAGCTAGCCGTTGGAGGCTTGAAGCTCTTATGTGGCGAGCTAACGAT	835
Qy	851	TAAGTAGACCGGCTGGGGAGTACGCGCGCAAGGTTAAACTCAATGAATTGACGGGGGC	910
Dh	836	TAAGTTAGACCGGCTGGGGAGTACGAGCGCAAGGTTAAACTCAATGAATTGACGGGGGC	895
Qy	911	CGCGAATACCGGTGAGCATGTGGTTTAAATTCGACGCAACCGCAAGAACTTAACTCACTAC	970
Dh	896	CGCGAATACCGGTGAGCATGTGGTTTAAATTCGAGCAAGCAAGCAAACTTAACTCAAGCC	955
Qy	971	TTGACATCCACAGAAACATTTAGAGAGATCAGATGGTGCTTCGGGAACTGTGACACAGTG	1030
Dh	956	TTGACATCCACAGAACTTTCCAGAGATGAGATGGGTGCTTCGGGAACTTGAAGACAGTG	1015
Qy	1031	CTGCAATGCGTGTGCTCAAGCTCGTGTGTGAATGTTGGTTAACTCCGTTAACGAGCGCA	1090
Dh	1016	CTGCAATGCGTGTGCTCAAGCTCGTGTGTGAATGTTGGTTAACTCCGTTAACGAGCGCA	1075
Qy	1091	ACCCCTGTCTCTTATTTGCGACGACGTAATGGTGGGAACTTAAAGAGACATGCCCGGTGAC	1150
Dh	1076	ACCCCTGTCTCTTATTTGACGACGTAATGGTGGGAACTTAAAGAGACTGCCCGGTGAC	1135
Qy	1151	AACCGAGAGAAAGTGGAGGACGACGTCAGTCATCATGACCCTTACAGATGAGGGCTACACA	1210
Dh	1136	AACCGAGAGAAAGTGGGAGTACGTCAGTCATCATAGCCCTTACGCGCTGGGCTACACACA	1195
Qy	1211	CGTGTACCAATGAGCGCTATACAGAGGGCTGCAGAGCTAGCGATAGCGAATCCACAAA	1270
Dh	1196	CGTGTACCAATGAGTGGGTATACAGAGGGTTGCCAAGCCGCGAGTGAGGCTTAATCCACAAA	1255
Qy	1271	GTAACGTGCTGATGTCGGAATTGGAATGCTGCAACTGCACTCCATGAAAGTCGGAATCGGTATTA	1330
Dh	1256	ACCGAATCGATGTCGGAATGCGAGTCGGAATTCGACTGCGTGAAGTCGGAATCGGTATTA	1315
Qy	1331	ATCGTGAATCACAATGTACAGGTGAATCGTTCGCGGCGCTTTATACACACCGCCGCTGAC	1390
Dh	1316	ATCGGCAATCACAATGTGCGCGTGAATACGTTCCCGGCGCTTTATACACACCGCCGCTGAC	1375
Qy	1391	ACCGATGGAGTTGATTTGCTCCAGAAATGACTAGCTTAAACCTTCGGGAAATGGCGTTTACC	1450
Dh	1376	ACCGATGGAGTTGATTTGCTCCAGAAATGACTAGCTTAAAC--TTCCGGGAGGACCGTTTACC	1433
Qy	1451	ACCGAATGTGCTCAATGACTGGGGTTGAAGTCTAC	1483
Dh	1434	ACCGAATGTGCTCAATGACTGGGGTTGAAGTCTAC	1466

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, RESULT 13
, US-10-286-787-5
, Sequence 5, Application US/10266787
, Publication No. US20030082777A1
, GENERAL INFORMATION:
, APPLICANT: Iano, Tetsuya
, APPLICANT: Imamura, Takeshi
, APPLICANT: Suda, Sakae
, APPLICANT: Homma, Tatsuomi
, TITLE OF INVENTION: Polyhydroxyalkanoate Synthase and Gene Encoding the Same Enzyme
, FILE REFERENCE: 03500.015225.3
, CURRENT APPLICATION NUMBER: US/10/266,787
, CURRENT FILING DATE: 2002-10-09
, PRIOR APPLICATION NUMBER: JP 2000-095004
, PRIOR FILING DATE: 2000-03-30
, NUMBER OF SEQ ID NOS: 11
, SOFTWARE: Microsoft Word
, SEQ ID NO 5

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[illegible]

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QY 1031 CTGCATGGCTGTCTGACGTGTGTGTGTGAAATGTTGGTTAAAGTCCGTTAAGCAGAGCGCA 1090
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Db 1434 ACGGAGTGTCAATGACTGCGGGTTGAAGTCTAC 1466

RESULT 14
US-10-252-518-5
Sequence 5, Application US/10252518
Publication No. US20030087413A1
GENERAL INFORMATION:
APPLICANT: Yano, Tetsuya
APPLICANT: Imamura, Takeshi
APPLICANT: Suda, Sakae
APPLICANT: Honma, Tsutomu
FILE OF INVENTION: Polyhydroxyalkanoate Synthase and Gene Encoding the Same Enzyme
CURRENT APPLICATION NUMBER: US/10/252,518
PRIOR FILING DATE: 2002-09-24
PRIOR APPLICATION NUMBER: JP 2000-095004
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Microsoft Word
SEQ ID NO 5
LENGTH: 1501
TYPE: DNA
ORGANISM: Pseudomonas jessenii P161, BP-7376
FEATURE:
FEATURE: cDNA to 16S rRNA
US-10-252-518-5

Query Match 76.1%; Score 1131; DB 15; Length 1501;
Best Local Similarity 88.2%; Freq. No. 1e-298;
Matches 1599; Conservative 0; Mismatches 165; Indels 9; Gaps 6;

QY 13 TGAACGCTGGCGGAGGCTTAACATGCAAGTCGAGCGGTAAACAGGAGGAGCTTCTCC 72
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QY 73 TGCTGACGAGCGGCGGAGCGGTGAGTAAACGCGTGAAGTCTGCTAGTAAAGGAGGACAA 132

Db 59 TGAATTC-AGCGCGAGCGGTGATGTAATGCTCTAGAAATCTGCTGTAGTGGGAGCA 117
QY 133 CATGTGAAAGAGATCTAATACCGATACGCGCTGAGGGGAAAGAGGGGACCTTCG 192
Db 118 CGTGTGAAAGAGGACCTAATACCGATACGCGCTGAGGGGAAAGAGGGGACCTTCG 175
QY 193 GAGCCTTCGCTATTAGATAGAGCTGCTGAGATTAGTATGTTGGTAAAGGCTTA 252
Db 176 GAGCCTTCGCTATTAGATAGAGCTGCTGAGATTAGTATGTTGGTAAAGGCTTA 235
QY 253 CCAAGCGAGAGATCTTAAGTGTCTGAGAGATGACAGTACACTGGGATGAGACAC 312
Db 236 CCAAGCGAGAGATCTTAAGTGTCTGAGAGATGATCATGCTCACTGGATGAGACAC 295
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QY 553 TAAAGCGCGGTGTAGTGTGTTGTTAAGTGGATGTGAAATCCAGAGGCTCAACTTGGAA 612
Db 536 TAAAGCGCGGTGTAGTGTGTTGTTAAGTGGATGTGAAATCCAGAGGCTCAACTTGGAA 595
QY 613 TGACACCGGATCTAGTGTAGTATGATGAGAGGGGTGTGAAATTCCTGTAGCG 672
Db 596 CTGATTCGAAATCTGACAGCTAGATAGTATGATGAGGGGTGTGAAATTCCTGTAGCG 655
QY 673 GTGAAATGCTAGTATATGAGAGAAATCATGAGTGGCGAAAGCGACACCTTGAATATC 732
Db 656 GTGAAATGCTAGTATATGAGAGAAATCATGAGTGGCGAAAGCGACACCTTGAATATC 715
QY 733 TGAACAGAGGTGCGAAAGGTGGGAGCAACAGATTAGTACCTGTGTGTCAGCC 792
Db 716 TGAACAGAGGTGCGAAAGGTGGGAGCAACAGATTAGTACCTGTGTGTCAGCC 775
QY 793 CGTAAACGATGTCTACAGCCGTTGG--GTTGTAATGACTTAAGTGGCGCAAGTAAACGCA 850
Db 776 CGTAAACGATGTCTACAGCCGTTGGAGCCTTGAAGCTCTTATGTTGGCGCAAGTAAACGCA 835
QY 851 TAAATAGACCGCTCTGGGAGTACGCGCGCAAGTTAACTCAATAGATTTGACGGGGCG 910
Db 836 TAAATAGACCGCTCTGGGAGTACGCGCGCAAGTTAACTCAATAGATTTGACGGGGCG 895
QY 911 CCGCACAAGCGGTGAGCATGTGTTAAATTCGAAACCAAGCGAAGAACCTTACTACTC 970
Db 896 CCGCACAAGCGGTGAGCATGTGTTAAATTCGAAACCAAGCGAAGAACCTTACTACTC 955
QY 971 TTGACATCCACAGAACATTTGAGAGATCAGATGTCCTTCGGGAATGTGAGACAGGTG 1030
Db 956 TTGACATCCATGAACTTTCCAGAGATGATGGGTGCTTCGGGAACTGTGAGACAGGTG 1015
QY 1031 CTGCATGGCTGTCTGACGTGTGTGTGTGAAATGTTGGTTAAAGTCCGTTAAGCAGAGCGCA 1090
Db 1016 CTGCATGGCTGTCTGACGTGTGTGTGTGAAATGTTGGTTAAAGTCCGTTAAGCAGAGCGCA 1075
QY 1091 ACCCTTGCTCTTATTTGGCCAGCAGCTAATGTTGGGAACTTTAAGAGACCTGCCGGTGA 1150
Db 1076 ACCCTTGCTCTTATTTGGCCAGCAGCTAATGTTGGGAACTTTAAGAGACCTGCCGGTGA 1135
QY 1151 AACCGAGAGAGGTGGGAGAGAGCTCAAGTCATCATGAGCCCTTACAGATGAGGCTTACACA 1210

Db 1136 AACCGGAGGAGGCTGGGATGACGTCAGTCACTATGCGCTTACGGCTGGCTACACA 1195
QY 1211 CGTGTACATGCGCTATACAGAGGCTGCAAGCTAGCGATAGTGAAGCCAGTCCACAA 1270
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QY 1271 GTAAGTGTGATGCTGGGATGAGTGTGCACTCCAGCTCCAGTGAAGTGGAGTGGTACTA 1330
Db 1256 ACCGATCGTATGCTGGATCGAGTGTGCACTCCAGCTCCAGTGAAGTGGAGTGGTACTA 1315
QY 1331 ATCGTGAATCAGAAATGTCACGGTGAATAGTTCGGGCGCTTGTACACACCGCCCTCAC 1390
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QY 1451 ACCGAGTGTGATGATGCTGGGCTTGAAGTCTAC 1483
Db 1434 ACGGTGTGATGATGATGCTGGGCTTGAAGTCTAC 1466

RESULT 15

US-10-105-305-1
; Sequence 1, Application US/10105305
; Publication No. US20030096182A1
; GENERAL INFORMATION:
; APPLICANT: CANON KABUSHIKI KAISHA
; TITLE OF INVENTION: POLYHYDROXYALKANONATE CONTAINING UNIT WITH THIENYL STRUCTURE IN THE
; TITLE OF INVENTION: CHAIN, PROCESS FOR ITS PRODUCTION, CHARGE CONTROL AGENT, TONER E
; TITLE OF INVENTION: TONER WHICH CONTAINS THIS POLYHYDROXYALKANONATE, AND IMAGE-FORMING
; TITLE OF INVENTION: IMAGE-FORMING APPARATUS WHICH MAKE USE OF THE TONER
; FILE REFERENCE: CRO16309
; CURRENT APPLICATION NUMBER: US/10/105,305
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: JP 2001-090026, JP 2001-133551
; PRIOR FILING DATE: 2001-3-27, 2001-4-27
; NUMBER OF SEQ ID NOS: 1
; SEQ ID NO 1
; LENGTH: 1501
; TYPE: DNA
; ORGANISM: Pseudomonas jessenii 161 strain.
US-10-105-305-1

Query Match 76.1%; Score 1131; DB 15; Length 1501;
Best Local Similarity 88.2%; Pred. No. 1e-298;
Matches 1299; Conservative 0; Mismatches 165; Indels 9; Gaps 6;

QY 13 TGAACGCTGGCGGCAAGCTTAAACACATGCAAGTCGAGCGGTACAGGGGAGCTTGTCTCC 72
Db 1 TGAACGCTGGCGGCAAGCTTAAACACATGCAAGTCGAGCGGTACAGGGGAGCTTGTCTCC 58
QY 73 TGGTGAACGAGCGGCGGAGCGGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 132
Db 59 TGAATTC-AACGCGGAGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 117
QY 133 CATGTGAAACCGATCTAATACCGATACGCTCTGAGGGGAAAGAGGGGACTCTTTCG 192
Db 118 CGTCTGAAAGGAGCGCTAATACCGATACGCTCTGAGGGGAAAGAGGGGACTCTTTCG 175
QY 193 GAGCTTCCGCTATTAGATGAGCTTGGATGATGATGATGATGATGATGATGATGATGATGATGAT 252
Db 176 GGGCTTGGCTTATGATGAGCTTGGATGATGATGATGATGATGATGATGATGATGATGATGAT 235
QY 253 CCAAGGCGAGATCTCTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 312
Db 236 CCAAGGCGAGATCTCTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 295
QY 313 GGGCCGAGCTCTTACGAGAGGCGAGCTGGGGAATTTGACAAATGGGCGCAAGCTGAT 372
Db 296 GGTCTCAAGCTCTTACGAGAGGCGAGCTGGGGAATTTGACAAATGGGCGCAAGCTGAT 355

QY 373 CCAGCATGCCCGCTGTGTGTAAGAAGCCCTTAGAGTTGTAAGCACTTTCAGGGGTGAGG 432
Db 356 CCAGCATGCCCGCTGTGTGTAAGAAGCTTTCAGATTTGTAAGCACTTTCAGGGGTGAGG 415
QY 433 AAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 492
Db 416 AAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 475
QY 493 CTCTGTGCAACACCCCGGTTAATACAGAGGTTGCAAGCTTAAATGGGAATTAATGAGGCG 552
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QY 851 TAAAGTGAACCCCTGGGAGTACCGCCGCAAGTTAAACTCAATGATGATGATGATGATGATGATGAT 910
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Mon Feb 2 10:57:11 2004

us-09-737-297-1.rnpb

Page 15

Db 1434 ACGGTGATTCATGACTGGGATGAGTCGTAC 1466

Search completed: January 31, 2004, 00:02:23
Job time : 570.517 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 30, 2004, 14:49:24 ; Search time 4084.5 Seconds

(without alignments)
10716.922 Million cell updates/sec

Title: US-09-737-297-2

Perfect score: 1070
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Scoring table: IDENTITY NUC

Gapop 10-0, Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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29: em_vl:*
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40: em_hgo_mus:*
41: em_hgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	1058	98.9	1457	1	AY014823 Pseudomon
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6	1057.6	98.8	1452	1	AY014828 Pseudomon
7	1057.2	98.8	1461	1	AF388208 Pseudomon
8	1057.2	98.8	1451	1	AY014824 Pseudomon
9	1056.6	98.7	1355	1	AF094729 Pseudomon
10	1056.4	98.7	1140	6	AX175617 Sequence
11	1056.4	98.7	1500	1	AF267911 Pseudomon
12	1054.8	98.6	1501	1	AF326356 Pseudomon
13	1054.4	98.5	1470	1	AY014825 Pseudomon
14	1051.6	98.3	1516	1	AF057645 Pseudomon
15	1051.2	98.2	1483	1	AF451270 Pseudomon
16	1050	98.1	1516	1	AF074384 Pseudomon
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18	1048.4	98.0	1452	1	AF320989 Pseudomon
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25	1044.8	97.6	1493	1	PCR244725 Pseudomon
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ALIGNMENTS

RESULT 1
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LOCUS AX175614 1070 bp DNA linear PAT 03-JUL-2001
DEFINITION Sequence 2 from Patent WO0144275.
ACCESSION AX175614
VERSION AX175614.1 GI:14598934
KEYWORDS
SOURCE
ORGANISM Pseudomonas sp.
Bacteria; Proteobacteria.

REFERENCE
AUTHORS Berry,M.J., Griffiths,A.U., Hill,P.J., Laybourne-Parry,J. and Mills,S.V.
TITLE Processes and organisms for the production of anti-freeze proteins
JOURNAL Patent: WO 0144275-A 2 21-JUN-2001;

FEATURES
source

Location/Qualifiers
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/db_xref="taxon:306"
/note="NCIMB 41076"

BASE COUNT 280 a 223 c 336 g 231 t
ORIGIN

Query Match 100.0%; Score 1070; DB 6; Length 1070;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1070; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 GAAGCTTGCTTCTTGAAGCGCGGAGCGGTGATATGCTTAGAATCTGCTTGCTA 120
DB 61 GAAGCTTGCTTCTTGAAGCGCGGAGCGGTGATATGCTTAGAATCTGCTTGCTA 120
QY 121 GTGCGGGGATPAGCTTGCGAAACGACGCTATATACCGCATACGCTTACGGGAAAGCAG 180
DB 121 GTGCGGGGATPAGCTTGCGAAACGACGCTATATACCGCATACGCTTACGGGAAAGCAG 180
QY 181 GGGACCTTGCGGCTTGCGCTATCAGATGAGCCTTAGGTCGATTAGTTGGTGAAGT 240
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QY 241 AATGGCTCACCAAGGGGAGCGATCCGTAATGCTGAGAGAGATGATCACTGACACTGAA 300
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RESULT 2
AY014829
LOCUS
DEFINITION
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VERSION
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GI:17220747
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Pseudomonas sp. NZ124
ORGANISM
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.

REFERENCE
1 (bases 1 to 1451)
Godfrey, S.A.C., Harrow, S.A., Marshall, J.W. and Klena, J.D.
Characterization of *Pseudomonas* species (sensu stricto) causing
'ginger blight' disease of cultivated *Agaricus bisporus* using 16S
RNA gene typing

JOURNAL
Unpublished
2 (bases 1 to 1451)
REFERENCE
Godfrey, S.A.C., Harrow, S.A., Marshall, J.W. and Klena, J.D.
Direct Submission
Submitted (28-NOV-2000) Integrated Crop Protection, Crop & Food
Research Ltd., Private Bag 4704, Christchurch 8152, New Zealand
TITLE
JOURNAL
location/Qualifiers

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 VERSION AY014815.1 GI:17220733
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 ORGANISM Pseudomonas sp. NZ065
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 Pseudomonadaceae; Pseudomonas.
 REFERENCE 1 (bases 1 to 1458)
 AUTHORS Godfrey, S.A.C., Harrow, S.A., Marshall, J.W. and Klena, J.D.
 TITLE Characterization of Pseudomonas species (sensu stricto) causing
 'ginger biotch' disease of cultivated Agave species using 16S
 rRNA gene typing
 JOURNAL Unpublished
 REFERENCES 2 (bases 1 to 1458)
 AUTHORS Godfrey, S.A.C., Harrow, S.A., Marshall, J.W. and Klena, J.D.
 TITLE Direct Submission
 JOURNAL Submitted (28-NOV-2000) Integrated Crop Protection, Crop & Food
 Research Ltd., Private Bag 4704, Christchurch 8152, New Zealand
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 Best Local Similarity 99.5%; Pred. No. 0;
 Matches 1061; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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 QY 483 CCGCTAACTGTGTCCAGACGCCCGGTATACAGAGGGTGCAGAGCTTAATCGAATTA 542
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 VERSION AY014823.1 GI:17220741
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 ORGANISM Pseudomonas sp. NZ106
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 Pseudomonadaceae; Pseudomonas.

REFERENCE 1 (bases 1 to 1467)
 Godfrey, S.A.C., Harrow, S.A., Marshall, J.W. and Klena, J.D.
 Characterization of *Pseudomonas* species (sensu stricto) causing
 'ginger blotch' disease of cultivated *Agaricus bisporus* using 16S
 rRNA gene typing

JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1467)
 Godfrey, S.A.C., Harrow, S.A., Marshall, J.W. and Klena, J.D.
 TITLE Direct Submission
 JOURNAL Submitted (28-NOV-2000) Integrated Crop Protection, Crop & Food
 Research Ltd., Private Bag 4704, Christchurch 8152, New Zealand

FEATURES
 Location/Qualifiers

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 Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 Pseudomonadaceae; Pseudomonas.

REFERENCE 1 (bases 1 to 1452)
 Godfrey, S.A., Harrow, S.A., Marshall, J.W. and Klena, J.D.
 Characterization by 16S rRNA sequence analysis of *Pseudomonas*
 causing 'blotch' disease of cultivated *Agaricus bisporus*

JOURNAL Appl. Environ. Microbiol. 67 (9), 4316-4323 (2001)
 MEDLINE 21417060
 PUBMED 11526038
 REFERENCE 2 (bases 1 to 1452)
 Godfrey, S.A.C., Harrow, S.A., Marshall, J.W. and Klena, J.D.
 TITLE Direct Submission
 JOURNAL Submitted (04-JUN-2001) Integrated Crop Protection, New Zealand

Institute for Crop & Food Research Ltd, Private Bag 4704,
Christchurch, New Zealand

FEATURES

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Location/Qualifiers

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DB 611 CTGGGAACTGCAATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 670
QY 663 TGTAGCGGTAAATGCTAGATATAGGAAGAAACACAGTGGCGAAGGACACACTGGA 722
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AY014828

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

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JOURNAL

AUTHORS

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AUTHORS

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BASE COUNT

369 a 320 c 451 g 311 t 1 others

ORIGIN

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98.8%; Score 1057.6; DB 1; Length 1452;

Best Local Similarity 99.4%; Pred. No. 0;

Matches 1060; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 3 CCTTGTCTAGATTGAACGCTGGCGGCGGCTTAACATGCAAGTCCAGCGGTAGAGAGA 62
DB 11 CCTGGCTCAGATTGAACGCTGGCGGCGGCTTAACATGCAAGTCCAGCGGTAGAGAGA 70
QY 63 AGCTTGTCTCTCTTGAAGCGGCGGCGGCTTAACATGCAAGTCCAGCGGTAGAGAGA 122
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QY 183 GACCTTCGGGCTTGGGCTATGAGATGAGACCTGAGTTCGGATTAGCTAGTGGTAGAGTAA 242
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 Db 611 CTGGGAATCTGCTCAAACTGACTGACTAGATAGTATGATGAGGTTGTTGAATTTCTG 670
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 Db 1031 ACAAGTGTGATGAGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1076

RESULT 7
 AF388208 1461 bp DNA linear ECT 15-JUN-2002
 LOCUS Pseudomonas sp. NZ064 16S ribosomal RNA gene, partial sequence.
 DEFINITION AF388208
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 VERSION AF388208.1 GI:18150370
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 ORGANISM Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas.
 REFERENCE 1 (bases 1 to 1461)
 AUTHORS Godfrey, S.A., Harrow, S.A., Marshall, J.W. and Klerna, J.D.
 TITLE Characterization by 16S rRNA sequence analysis of pseudomonads causing blotch disease of cultivated Agaricus bisporus
 JOURNAL Appl. Environ. Microbiol. 67 (9), 4316-4323 (2001)
 MEDLINE 21417060
 PUBMED 11526038
 REFERENCE 2 (bases 1 to 1461)

AUTHORS Godfrey, S.A.C., Harrow, S.A., Marshall, J.W. and Klerna, J.D.
 TITLE Direct Submission
 JOURNAL Submitted (04-JUN-2001) Integrated Crop Protection, New Zealand
 INSTITUTE for Crop & Food Research Ltd, Private Bag 4704,
 Christchurch, New Zealand
 FEATURES
 source 1. 1461
 /organism="Pseudomonas sp. NZ064"
 /mol_type="genomic DNA"
 /strain="NZ064"
 /db_xref="taxon:183774"
 <1..21461
 /product="16S ribosomal RNA"
 BASE COUNT 372 a 323 c 453 g 311 t 2 others
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 Query Match 98.8%; Score 1057.2; DB 1; Length 1461;
 Best Local Similarity 99.3%; Pred. No. 0;
 Matches 1059; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 QY 3 CCTTGCTCAGATTGAACGCTGCGCGAGGCTTAACATGCAAGTCGACGGTAGAGA 62
 Db 11 CTTGCTCAGATTGAACGCTGCGCGAGGCTTAACATGCAAGTCGACGGTAGAGA 70
 QY 63 AGCTTGCTTCTCTGAGAGCGCGGAGCGGATGATATGCTAGAAATCTGCTGTAGT 122
 Db 71 AGCTTGCTTCTCTGAGAGCGCGGAGCGGATGATATGCTAGAAATCTGCTGTAGT 130
 QY 123 GGGGGATTAAGTTCGGAACCGGACGCTATACCGCTACGCTTACGGGAAAGCAAGG 182
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 QY 243 TGGCTACCAAGCGGACGATCCGTAACTGCTTGAAGAGATGATAGTCACTGGAAT 302
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Db 721 CTGAGTGTGCGAAGCGT 780
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Db 781 ACGATGTCACTAGCCGTTGTGAAGCCTTGTAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 840
Qy 855 TGACCGCGCTGGGGAGTACGGCGCCGCAAGTTAAACTCAATGTGAAGCGGGCGCCGCA 914
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Db 1021 TGCGT 1054

RESULT 15
US-10-266-787-5
Sequence 5, Application US/10266787
Publication No. US20030082777A1
GENERAL INFORMATION:
APPLICANT: Iano, Tetsuya
APPLICANT: Imamura, Takeshi
APPLICANT: Honda, Sakae
APPLICANT: Horita, Sada
TITLE OF INVENTION: Polyhydroxyalkanoate Synthase and Gene Encoding the Same Enzyme
FILE REFERENCE: 03500.015225.3
CURRENT FILING DATE: 2002-10-09
PRIORITY FILING DATE: 2000-03-30
PRIORITY FILING DATE: 2000-03-30
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Microsoft Word
SEQ ID NO 5
LENGTH: 1501
TYPE: DNA
ORGANISM: Pseudomonas jessenii Pl61 ; BP-7376
FEATURE:
FEATURE: CDNA to 16S rRNA
US-10-266-787-5

Query Match 92.1%; Score 985.2; DB 15; Length 1501;
Best Local Similarity 95.9%; Pred. No. 1.3e-292;
Matches 1011; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

Qy 15 TGAACGCTGCGCGAGGCTTAACATGCAAGTCAGCGGTAGAGGAAGCTTGCTTGC 74
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Db 661 ATGCGTAGATATAGGAAGCAACCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 720
Qy 735 CTGAGTGTGCGAAGCGT 794
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Search completed: January 31, 2004, 00:02:25
Job time : 408.483 secs

SOFTWARE: Patentin version 3.1
; SEQ ID NO 1
; LENGTH: 1501
; TYPE: DNA
; ORGANISM: Pseudomonas jessenii 161 strain
US-10-411-319-1

Query Match 92.1%; Score 985.2; DB 13; Length 1501;
Best Local Similarity 95.9%; Pred. No. 1.3e-292;
Matches 1011; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

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RESULT 14

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; Sequence 5, Application US/10218519
; Publication No. US20030049806A1
; GENERAL INFORMATION:
; APPLICANT: Yano, Tetsuya
; APPLICANT: Imamura, Takeshi
; APPLICANT: Suda, Sakae
; APPLICANT: Honma, Tsutomu
; TITLE OF INVENTION: Polyhydroxyalkanoate Synthase and Gene Encoding the Same Enzy
; FILE REFERENCE: 03500 015225.1
; CURRENT FILING DATE: 2001-03-30
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Microsoft Word
; SEQ ID NO 5
; LENGTH: 1501
; TYPE: DNA
; ORGANISM: Pseudomonas jessenii P.161 ; BP-7376
; FEATURE:
; FEATURE: CDNA to 16S rRNA
US-10-218-519-5
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Query Match 92.1%; Score 985.2; DB 15; Length 1501;
Best Local Similarity 95.9%; Pred. No. 1.3e-292;
Matches 1011; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

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OY	915	CAAGCGGTGGAGCATGTGTATTATTCGAAGCAACGCCAACAACCTTACCGAGCTTGAC	974
Dd	901	CAAGCGGTGGAGCATGTGTATTATTCGAAGCAACGCCAACAACCTTACCGAGCTTGAC	960
OY	975	ATCCATGAATTTCTTAGAGATGATTTGTGCTTCGGGAACATTGAGACAGTGTGCA	1034
Dd	961	ATCCATGAATTTCTTAGAGATGATTTGTGCTTCGGGAACATTGAGACAGTGTGCA	1020
OY	1035	TGGCTGTGCTCAGCTCGTGTGTGTGAATGTAGG	1068
Dd	1021	TGGCTGTGCTCAGCTCGTGTGTGTGAATGTGGG	1054
RESULT 12			
US-10-242-696-1			
Sequence 1, Application US/107242696			
Publication No. US20030180899A1			
GENERAL INFORMATION:			
APPLICANT: Honma, Tsutomu			
APPLICANT: Kodayashi, Toyoko			
APPLICANT: Yano, Tetsuya			
APPLICANT: Kobayashi, Shin			
APPLICANT: Imamura, Takeshi			
APPLICANT: Suda, Sakae			
TITLE OF INVENTION: Process for producing polyhydroxyalkanoate by utilizing microorgans			
FILE REFERENCE: 03500, 015010.1			
CURRENT APPLICATION NUMBER: US/10/242, 696			
CURRENT FILING DATE: 2002-09-13			
PRIOR APPLICATION NUMBER: JP 11-371864			
PRIOR FILING DATE: 12-27-1999			
PRIOR APPLICATION NUMBER: JP 11-371867			
PRIOR FILING DATE: 12-27-1999			
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PRIOR FILING DATE: 12-27-1999			
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PRIOR FILING DATE: 01-31-2000			
PRIOR APPLICATION NUMBER: JP 2000-023025			
PRIOR FILING DATE: 01-31-2000			
PRIOR APPLICATION NUMBER: JP 2000-361323			
PRIOR FILING DATE: 11-28-2000			
NUMBER OF SEQ ID NOS: 1			
SOFTWARE: Microsoft Word			
SEQ ID NO 1			
LENGTH: 1501			
TYPE: DNA			
ORGANISM: Pseudomonas jessenii Pl61 ; EERM P-17445			
US-10-242-696-1			
Query Match 92.1%; Score 885.2; DB 13; Length 1501;			
Best Local Similarity 95.9%; Pred. No. 1,3e-292;			
Matches 1011; Conservative 0; Mismatches 43; Indels 0; Gaps 0;			
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OY	75	TTGAGAGCGGCGGAGCGGCTGAGTATGCGCTAGCAATGCTGCTGTAGTGGGGATAAGT	134
Dd	61	AATTCAGGGCGGAGCGGCTGAGTATGCGCTAGCAATGCTGCTGTAGTGGGGATAAGT	120
OY	135	TCGGAACGGAGCGTTAAATACCGCATAGCTCTTAAGGGAGAAAAGACAGGGAACCTTCGGGCC	194
Dd	121	CTCGAAGGGAGCGCTTAATACCGCATAGCTCTTAAGGGAGAAAAGACAGGGAACCTTCGGGCC	180
OY	195	TTGGCGTATCAGATAGAGCTTAGTGGATTAGTGTAGAGTATGAGCTCACCAAG	254

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Db      181  TTGGCGATCATGATGAGACCTAGGTCGGATTAGCTAATTGGTGGAGTAAATGGCTACCAAG 240
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Db      241  GCGACGATCCGTAATCTGTCGTGAGAGATGATCAATGTCACATGGAACCTGAGACACGGTCC 300
QY      315  AGACTCCTACGGGAGGAGCAGTCGTGGGAAATATTGACCAATGGCGGAAGCCTGATCCAG 374
Db      301  AGACTCCTACGGGAGGAGCAGTCGTGGGAAATATTGACCAATGGCGGAAGCCTGATCCAG 360
QY      375  CATGCCGCGTGTGGAAGAAAGTCTCCGATTGTGTAAAGCACTTTAGTTGGGAGGAAGG 434
Db      361  CATGCCGCGTGTGGAAGAAAGTCTCCGATTGTGTAAAGCACTTTAGTTGGGAGGAAGG 420
QY      435  TTGTAGATTAAACTCTGCATTTTGAACGTTTACCGACAGATTAAGCACCGGCTAACTCTG 494
Db      421  CATTAACCTTAATCGTAGTGTGTTTACGTTTACCGACAGATTAAGCACCGGCTAACTCTG 480
QY      495  TGCCAGACGCGCGGTATATCAAGAGGTGCAACGCTTATTCGGAATTAATGGGCGTAAAG 554
Db      481  TGCCAGACGCGCGGTATATCAAGAGGTGCAACGCTTATTCGGAATTAATGGGCGTAAAG 540
QY      555  CGCGCGTAGGTGGTGTGTTTAAATTGATGGAGTGAATATCCCGGCGTCAACCTGGGAACTGCA 614
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QY      615  TTCAAACTGACCTGACCTAGAGTATGGTAGAGGGTGGTGAATTTCTGTGTGACGGTGA 674
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QY      675  ATGCGTATATATGGAAGAAACACACAGTGGCGGAAGCGAACCACTTGAATTAATCTGACA 734
Db      661  ATGCGTATATATGGAAGAAACACACAGTGGCGGAAGCGAACCACTTGAATTAATCTGACA 720
QY      735  CTGAGGTGCGAAAGCGTGGGAGCAACAACAGATTAATATCCCTGTAGTCCACCGCGTAA 794
Db      721  CTGAGGTGCGAAAGCGTGGGAGCAACAACAGATTAATATCCCTGTAGTCCACCGCGTAA 780
QY      795  ACGATGTCAACTAGCCGTTTGAAGCCCTTGACTTTTAAATGTTGGCGACGTAACGATTAA 854
Db      781  ACGATGTCAACTAGCCGTTTGAAGCCCTTGACTTTTAAATGTTGGCGACGTAACGATTAA 840
QY      855  TGAACCGCTGGGAGATGACGCGCGCAAGTTTAAACTCAATGAAATGACGGGGGCCCGCA 914
Db      841  TGAACCGCTGGGAGATGACGCGCGCAAGTTTAAACTCAATGAAATGACGGGGGCCCGCA 900
QY      915  CAAGCGGTGAGAGCATGTGTTTAATTCGAAGCAACGCGGAAGAACTTACAGGCTTTCAG 974
Db      901  CAAGCGGTGAGAGCATGTGTTTAATTCGAAGCAACGCGGAAGAACTTACAGGCTTTCAG 960
QY      975  ATCCAAATGAACCTTCTAAGATATGATGTGGCTTGGGAAACCTGAGACAGGTGTGCA 1034
Db      961  ATCCAAATGAACCTTCTAAGATATGATGTGGCTTGGGAAACCTGAGACAGGTGTGCA 1020
QY      1035  TGCGTGTGTCAGCTCGTGTGTGTGAATGTAAAG 1068
Db      1021  TGCGTGTGTCAGCTCGTGTGTGTGAATGTGTGG 1054

RESULT 13
US-10-411-319-1
; Sequence 1, Application US/10411319
; Publication No. US20030208029A1
; GENERAL INFORMATION:
; APPLICANT: Canon Inc.
; TITLE OF INVENTION: Polyhydroxynate, Method For Production Thereof And Microorganism
; FILE REFERENCE: 03500.015001.1
; CURRENT APPLICATION NUMBER: US/10/411.319
; PRIORITY FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: US 09/748,205
; PRIORITY FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 1

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Db	61	AATTCAAGCGGAGCGAGTGTAGTAAATGCTTAAGAAATCTGCTGGTATGTGGGGACAAACGT	120
QY	135	TGGGAACCGAACCGCTAATACCGGATACGTTCTTACCGGGAGAAAGCAGGGGACCTTCCGAGCC	194
Db	121	CTGCAAAAGGAGCCCTAATACCGGATACGTTCTTACCGGGAGAAAGCAGGGGACCTTCCGAGCC	180
QY	195	TTGGCGATCAGATGAGACCTAGGTCCGATTTAGCTAGTGGTGAAGTAAATGGCTCAGCAAG	254
Db	181	TTGGCGATCAGATGAGACCTAGGTCCGATTTAGCTAGTGGTGAAGTAAATGGCTCAGCAAG	240
QY	255	GCGACGATCCGTAACCTGGTCTGAGAGATGATCACTGACACCTGAACTGAGACCGGTCC	314
Db	241	GCGACGATCCGTAACCTGGTCTGAGAGATGATCACTGACACCTGAACTGAGACCGGTCC	300
QY	315	AGACTCCTACGGGAGGACAGATGGGGAAATATGGACAAATGGGGAAAGCCTAATCCAC	374
Db	301	AGACTCCTACGGGAGGACAGATGGGGAAATATGGACAAATGGGGAAAGCCTAATCCAC	360
QY	375	CATCCCGCGTGTGTGAAAGAGTCTTCGATTTGTAACACTTTAACTTGGAGAGAGG	434
Db	361	CATCCCGCGTGTGTGAAAGAGTCTTCGATTTGTAACACTTTAACTTGGAGAGAGG	420
QY	435	TTTGAGATTAACTCTGCAATTTTGAAGCTTACGACAGATTAAGCACCGGCTAATCTTG	494
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QY	495	TGCCAGACGCGCGGTATATACAGAGGTGCAAAGCCTTATCGAATTAACGGGCTTAAG	554
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Db	601	TTCAAACTGACCTAAGCTAAGATATGTGAGAGGTGTGGAATTTCTGTGTACCGGTGA	660
QY	675	ATGCGTAGATATAGGAAGGACACCAAGTGGGAAAGGAGGACCTCGACTAATATGACA	734
Db	661	ATGCGTAGATATAGGAAGGACACCAAGTGGGAAAGGAGGACCTCGACTAATATGACA	720
QY	735	CTGAGGTGCGAAAGCGTGGGGAGCAAAACAGATTAGATCCTTGGTATGTCCAGCGCTTA	794
Db	721	CTGAGGTGCGAAAGCGTGGGGAGCAAAACAGATTAGATCCTTGGTATGTCCAGCGCTTA	780
QY	795	ACGATGTCAACTAGCCGTTGAAAGCCTTAGCTTTTATGGTCGAGCTAACGATTAAGT	854
Db	781	ACGATGTCAACTAGCCGTTGAAAGCCTTAGCTTTTATGGTCGAGCTAACGATTAAGT	840
QY	855	TGACCCGCTGGGGAGTACGCGCGCAAGGTTAAAACTCAATGAATTGACGGGGGCCCGCA	914
Db	841	TGACCCGCTGGGGAGTACGCGCGCAAGGTTAAAACTCAATGAATTGACGGGGGCCCGCA	900
QY	915	CAAGCGGTGAGATGTGGTTTAATTGCAACCAACGGGAACCTTACCAAGCCTTGAC	974
Db	901	CAAGCGGTGAGATGTGGTTTAATTGCAACCAACGGGAACCTTACCAAGCCTTGAC	960
QY	975	ATCCAATGAACCTTTCAGAGATGAATGTGCTCTTCGGGAACAATTGACACAGTGTGTGA	1034
Db	961	ATCCAATGAACCTTTCAGAGATGAATGTGCTCTTCGGGAACAATTGACACAGTGTGTGA	1020
QY	1035	TGGCTGTGCAAGCTCGTGTGTGTAAGTAAG	1068
Db	1021	TGGCTGTGCAAGCTCGTGTGTGTAAGTAAG	1054

```

: APPLICANT: Canon Inc.
: TITLE OF INVENTION: Polyhydroxyalkanoate containing 3-hydroxybenzoylalcanoic acid
: TITLE OR INVENTION: monomer unit, and method for producing the same.
: FILE REFERENCE: 4396021
: CURRENT APPLICATION NUMBER: US/09/791,610
: CURRENT FILING DATE: 2002-09-30
: NUMBER OF SEQ ID NOS: 1
: SEQ ID NO 1
: LENGTH: 1501
: TYPE: DNA
: ORGANISM: Pseudomonas jesseni 161 strain.
: US-09-791-610-1

```

Query Match	92.1%;	Score 985.2;	DB 11;	Length 1501;
Post Total Similarity	92.08;	Score 985.1;	DB 11;	Length 1501;

QY	1	TGAACGCTGGCGGACGGCCCTAACACATGCAAGTGGACGGGTAGAGAGAACTTGCTTC	74
Db	1	TGAACGCTGGCGGACGGCCCTAACACATGCAAGTGGACGGGTAGAGAGAACTTGCTTC	60
QY	75	TTGAGAGCGCGGACGGGTGAATATGCTTAGAATCTGCCTGTAGTGGGGTAACGT	134
Db	61	AATTCAAGCGCGGACGGGTGAATATGCTTAGAATCTGCCTGTAGTGGGGTAACAGT	120
QY	135	TGGAAACGGAAGCTTATTCGGCATACGCTCTAACGGGAAAGCAGGGGACCTTCGGGCC	194
Db	121	CTGGAAAGGGAAGCTTATTCGGCATACCTCTAACGGGAAAGCAGGGGACCTTCGGGCC	180
QY	195	TTGCGCTATCAGATGAGGCTAGTGGATTTGACGTAGTGGTGGGTAAATGGCTCACCAAG	254
Db	181	TTGCGCTATCAGATGAGGCTAGTGGATTTGACGTAGTGGTGGGTAAATGGCTCACCAAG	240
QY	255	GCGACGATCCGTAACTGGTCTGAGAGATGATCACTCAACTGGAATGAGACACCGTCC	314
Db	241	GCGACGATCCGTAACTGGTCTGAGAGATGATCACTCAACTGGAATGAGACACCGTCC	300
QY	315	AGACTCTTACGGGAGGCAAGCAGTGGGAAATTTGGACATAGGGCGAAAGCTTATCCAGC	374
Db	301	AGACTCTTACGGGAGGCAAGTGGGAAATTTGGACATAGGGCGAAAGCTTATCCAGC	360
QY	375	CATGCCGCTGTGTAAAGAGAGTCTTCGGATTTGTAAGCACTTAAATTGGGAGAGAGG	434
Db	361	CATGCCGCTGTGTAAAGAGAGTCTTCGGATTTGTAAGCACTTAAATTGGGAGAGAGG	420
QY	435	TTGTAGATTAACTCTCGCAATTTTGACGTTACCGACAGATAAGCACCGGCTAACTGTG	494
Db	421	CATTAACTTAATACCTTAGTGTGTTTGAAGTTACCGACAGATAAGCACCGGCTAACTGTG	480
QY	495	TGCGACACACCGCGGTAAATACAGAGGGTGCAGAGCTTAATCCGAATTAATCTGGGCGTAAAG	554
Db	481	TGCGACACACCGCGGTAAATACAGAGGGTGCAGAGGTAAATCCGAATTAATCTGGGCGTAAAG	540
QY	555	CGGCGGTAGTGGTTGTAAAGTTGAGATGTGAAATCCCGGGCTCAACTGGGAACTGCA	614
Db	541	CGGCGGTAGTGGTTGTAAAGTTGAGATGTGAAACCCCGGGCTCAACTGGGAACTGCA	600
QY	615	TTCAAAACTGACTGACTAGATATGATAGAGGGTGTGGAAATTTCTGTGTACCGGTGA	674
Db	601	TTCAAAACTGAAAGCTAGATATGATAGAGGGTGTGGAAATTTCTGTGTACCGGTGA	660
QY	675	ATGCGTAGATATAGGAAGGAACACACAGTGGGAAAGGAGCACCTGAGACTAATACTGACA	734
Db	661	ATGCGTAGATATAGGAAGGAACACACAGTGGGAAAGGAGCACCTGAGACTGATCTGACA	720
QY	735	CTGAGGTGCGAAAGCGTGGGAGCAACAGGATTAGTACCCTGTGTAGTCCAGCCGTAA	794
Db	721	CTGAGGTGCGAAAGCGTGGGAGCAACAGGATTAGTACCCTGTGTAGTCCAGCCGTAA	780
QY	795	ACGATGTCAACAGCCGTGGAACCTTGAGCTTTTAATGGCGGCACTAACGATTAAT	854
Db	781	ACGATGTCAACAGCCGTGGAACCTTTAGTGGCGCACTAACGATTAAT	840

Db 841 TGACCGCTGGAGTACGCGCCGAGGTTAAACTCAATGATTTGACGGGGGCCCGCA 900
Qy 915 CAAGCGGTGAGCATGTGTTTAAATTCGAAAGCAACCGAAACCTTACAGGCTTGAC 974
Db 901 CAAGCGGTGAGCATGTGTTTAAATTCGAAAGCAACCGAAACCTTACAGGCTTGAC 960
Qy 975 ATCCAAATGAACCTTCTAGAGATGATGAGTGGCTTGGGAAACATTTAGACAGGTGCTGA 1034
Db 961 ATCCAAATGAACCTTCTAGAGATGATGAGTGGCTTGGGAAACATTTAGACAGGTGCTGA 1020
Qy 1035 TGAGTGTGCTACGCTGCTGTTTGAATGTAAG 1068
Db 1021 TGAGTGTGCTACGCTGCTGTTGAGATGTTGGG 1054

RESULT 9

US-09-793-920A-1
Sequence 1, Application US/09793920A
Patent No. US20020065389A1
GENERAL INFORMATION:
APPLICANT: Canon Inc.
TITLE OF INVENTION: Polyhydroxyalkanoate containing 3-hydroxyphenylalkanoic acid as
FILE REFERENCE: 4396021
CURRENT FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 1
SEQ ID NO 1
LENGTH: 1501
TYPE: DNA
ORGANISM: Pseudomonas jessenii 161 strain.
US-09-793-920A-1

Query Match 92.1%; Score 985.2; DB 9; Length 1501;
Best Local Similarity 95.9%; Pred. No. 1.3e-292;
Matches 1011; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

Qy 15 TGAACGCTGGCGGAGGCTTAACATGACATGACGCGTGAAGAGAAAGCTTCTTC 74
Db 1 TGAACGCTGGCGGAGGCTTAACATGACATGACGCGTGAAGAGAAAGCTTCTTC 60
Qy 75 TTGAGAGCGGCGGAGCGGTGAGTAAGTCCCTAGGAATCTGCTGATGAGGAGTAAAGT 134
Db 61 AATTACGCGGCGGAGCGGTGAGTAAGTCCCTAGGAATCTGCTGATGAGGAGTAAAGT 120
Qy 135 TCGAAAAGGAGCGCTAATACCGCATACGTCCTACGCGAGAAAGCAAGGAGCTTCGGGCC 194
Db 121 CTGAAAAGGAGCGCTAATACCGCATACGTCCTACGCGAGAAAGCAAGGAGCTTCGGGCC 180
Qy 195 TTGCGCTATCAGATGAGCTTAAGTCCGATTAGCTAGTGGTGAAGTAATGGCTACCAAG 254
Db 181 TTGCGCTATCAGATGAGCTTAAGTCCGATTAGCTAGTGGTGAAGTAATGGCTACCAAG 240
Qy 255 GCGAGATCCGTAATCGTCTGAGAGAGATGATCAGTCAACCTAGAACTGAGACAGGTCC 314
Db 241 GCGAGATCCGTAATCGTCTGAGAGAGATGATCAGTCAACCTAGAACTGAGACAGGTCC 300
Qy 315 AGACTCTTACGAGAGGAGCAGAGTGGGGAATTTGACAAATGGGCGAAAGCTTGATCCAGC 374
Db 301 AGACTCTTACGAGAGGAGCAGAGTGGGGAATTTGACAAATGGGCGAAAGCTTGATCCAGC 360
Qy 375 CATGCGCGTGTGTAAGAGAGTCTTGATGTAAGCACTTTAAGTGGGAGAGAGG 434
Db 361 CATGCGCGTGTGTAAGAGAGTCTTGATGTAAGCACTTTAAGTGGGAGAGAGG 420
Qy 435 TTGAGATTAATACCTGCAATTTTGAAGTTCAGTCCGACAGAAATAGCAGCGCTAACTCTG 494
Db 421 CATTAACCTTAATACCTGCAATTTTGAAGTTCAGTCCGACAGAAATAGCAGCGCTAACTCTG 480
Qy 495 TGCAGAGCGCGCGGTATATCAGAGGAGTGAAGCGTTAATCGAATTAATCTGGGCGTAAAG 554
Db 481 TGCAGAGCGCGCGGTATATCAGAGGAGTGAAGCGTTAATCGAATTAATCTGGGCGTAAAG 540

Qy 555 CGAGCGTATGAGTGTGTTGTAAGTGAATGTGAATCCCGGGGCTCAACCTGAGAACTGCA 614
Db 541 CGAGCGTATGAGTGTGTTGTAAGTGAATGTGAATCCCGGGGCTCAACCTGAGAACTGCA 600
Qy 615 TTCAAACTGACTGACTAGAGTATGATGAGGAGGTGTAATTTCTGTGATGAGGTGAA 674
Db 601 TTCAAACTGACTGACTAGAGTATGATGAGGAGGTGTAATTTCTGTGATGAGGTGAA 660
Qy 675 ATCCGTAATATGAGAGAGAACACAGTGGCGCAAGGAGCAACCTGAGCTAATCTGCA 734
Db 661 ATCCGTAATATGAGAGAGAACACAGTGGCGCAAGGAGCAACCTGAGCTAATCTGCA 720
Qy 735 CTGAGTGGGAAAGCGTGGGAGCAACAGATTGATACCTGATGCTCCAGCGGTAA 794
Db 721 CTGAGTGGGAAAGCGTGGGAGCAACAGATTGATACCTGATGCTCCAGCGGTAA 780
Qy 795 ACATGTCACTAATCCCTGTTGAAGCTTGAAGCTTTAATGAGGAGCTTAATGATAGT 854
Db 781 ACATGTCACTAATCCCTGTTGAAGCTTGAAGCTTTAATGAGGAGCTTAATGATAGT 840
Qy 855 TGACCGCTGGGAGAGTACGCGCGCAAGGTTAACTCAATGAAATGAAATGAGGAGCGCGCA 914
Db 841 TGACCGCTGGGAGAGTACGCGCGCAAGGTTAACTCAATGAAATGAAATGAGGAGCGCGCA 900
Qy 915 CAAGCGGTGAGCATGTGTTTAAATTCGAAAGCAACCGAAACCTTACAGGCTTGAC 974
Db 901 CAAGCGGTGAGCATGTGTTTAAATTCGAAAGCAACCGAAACCTTACAGGCTTGAC 960
Qy 975 ATCCAAATGAACCTTCTAGAGATGATGAGTGGCTTGGGAAACATTTAGACAGGTGCTGA 1034
Db 961 ATCCAAATGAACCTTCTAGAGATGATGAGTGGCTTGGGAAACATTTAGACAGGTGCTGA 1020
Qy 1035 TGAGTGTGCTACGCTGCTGTTTGAATGTAAG 1068
Db 1021 TGAGTGTGCTACGCTGCTGTTGAGATGTTGGG 1054

RESULT 10

US-09-951-720-1
Sequence 1, Application US/09951720
Patent No. US20020160467A1
GENERAL INFORMATION:
APPLICANT: Canon Kabushiki Kaisha
TITLE OF INVENTION: Polyhydroxyalkanoate and Manufacturing Method Thereof
FILE REFERENCE: 4477001
CURRENT FILING DATE: 2000-09-14
PRIORITY FILING DATE: 2000-09-14
PRIORITY APPLICATION NUMBER: JP 279900/2000
JP 378827/2000
JP 165238/2001
JP 165509/2001
JP 275063/2001
PRIORITY FILING DATE: 2000-09-14
PRIORITY FILING DATE: 2000-12-13
2001-05-31
2001-05-31
2001-09-11
NUMBER OF SEQ ID NOS: 1
SEQ ID NO 1
LENGTH: 1501
TYPE: DNA
ORGANISM: Pseudomonas jessenii 161 strain.
US-09-951-720-1

Query Match 92.1%; Score 985.2; DB 10; Length 1501;
Best Local Similarity 95.9%; Pred. No. 1.3e-292;
Matches 1011; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

Qy 15 TGAACGCTGGCGGAGGCTTAACATGACATGACGCGTGAAGAGAAAGCTTCTTC 74
Db 1 TGAACGCTGGCGGAGGCTTAACATGACATGACGCGTGAAGAGAAAGCTTCTTC 60
Qy 75 TTGAGAGCGGCGGAGCGGTGAGTAATGCTTGAAGATCTGCTGATGAGGAGTAAAGT 134

QY 795 ACGATGTCAACTACCGCTTGGAAAGCCTTGAAGCTTTTATGTGGCGAGCTTAACGCACTTAAGT 854
DB 781 ACGATGTCAACTACCGCTTGGAAAGCCTTGAAGCTTTTATGTGGCGAGCTTAACGCACTTAAGT 840
QY 855 TGACCGCTGCGGGAGTACCGCGCGCAAGGTTAAACCAATGAATTTAGCGGGCGCCGCCA 914
DB 841 TGACCGCTGCGGGAGTACCGCGCGCAAGGTTAAACCAATGAATTTAGCGGGCGCCGCCA 900
QY 915 CAAGCGGTGAGCATGTGTTTAAATTCGAAGCAACCGCAAGAACTTACCAAGCCTTAGC 974
DB 901 CAAGCGGTGAGCATGTGTTTAAATTCGAAGCAACCGCAAGAACTTACCAAGCCTTAGC 960
QY 975 ATCCATGAACCTTTCAAGATAGATGTGGGCTTGGGAAACATTTGAGAGAGAGTGTCTCA 1034
DB 961 ATCCATGAACCTTTCAAGATAGATGTGGGCTTGGGAAACATTTGAGAGAGAGTGTCTCA 1020
QY 1035 TGCGTGTCTGACGCTGCTGTGTGAATGTAAG 1068
DB 1021 TGCGTGTCTGACGCTGCTGTGTGAATGTTGGG 1054

RESULT 6
US-09-745-476-1
; Sequence 1, Application US/09745476
; Patent No. US20010029039A1
; GENERAL INFORMATION:
; APPLICANT: CANON INC.
; TITLE OF INVENTION: Preparation of Poly-hydroxyalkanoic Acid
; FILE REFERENCE: 4351008
; CURRENT APPLICATION NUMBER: US/09/745,476
; CURRENT FILING DATE: 2000-12-26
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Microsoft Word
; SEQ ID NO: 1
; LENGTH: 1501
; TYPE: DNA
; ORGANISM: Pseudomonas jessenii P161 ; FERM P-17445
US-09-745-476-1

Query Match 92.1%; Score 985.2; DB 9; Length 1501;
Best Local Similarity 95.9%; Pred. No. 1.3e-292;
Matches 1011; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 15 TGAACGCTGCGGCGGAGCCTTAACATGCAATGCAAGTCGAGCGGTAGAGAGAACTTGTCTTC 74
DB 1 TGAACGCTGCGGCGGAGCCTTAACATGCAATGCAAGTCGAGCGGTAGAGAGAACTTGTCTTC 60
QY 75 TTGAGAGCGGCGGAGCGGTGAGTAATGCTCTAGGAATCTGCTGTAAGTGGGGGATAAGCT 134
DB 61 AATTCAAGCGGCGGAGCGGTGAGTAATGCTCTAGGAATCTGCTGTAAGTGGGGGATAAGCT 120
QY 135 TCGAAAACGAGCGCTAATACCGCATACGCTCTACCGGAGAAAGCAAGGAGACCTTCGAGCC 194
DB 121 CTCGAAAGGAGCGCTAATACCGCATACGCTCTACCGGAGAAAGCAAGGAGACCTTCGAGCC 180
QY 195 TTGCGCTATCAGATGAGCGCTAAGTCCGATTAAGTCTAGTGTGTAGGTAATGCTACCAAG 254
DB 181 TTGCGCTATCAGATGAGCGCTAAGTCCGATTAAGTGTGTAGGTAATGCTACCAAG 240
QY 255 GCGAGCATCCGTAATGATGCTGTGAGAGATGATCACTGCACTGCAAGCTGAGCAAGCGGCTC 314
DB 241 GCGAGCATCCGTAATGATGCTGTGAGAGATGATCACTGCACTGCAAGCTGAGCAAGCGGCTC 300
QY 315 AGACTCTTACGGAGGAGGAGAGATGAGGGAATTTGACATAGGCGCAAAAGCTGATCCAGC 374
DB 301 AGACTCTTACGGAGGAGGAGAGATGAGGGAATTTGACATAGGCGCAAAAGCTGATCCAGC 360
QY 375 CATGCCGCTGTGTGAAGAAGGCTTCGATTTGAAGCACTTAAGTTGGAGGAGAGG 434
DB 361 CATGCCGCTGTGTGAAGAAGGCTTCGATTTGAAGCACTTAAGTTGGAGGAGAGG 420
QY 435 TTGTAGATTAACTCTGCAATTTTGAAGTTACCGAGCATTAAGCAACCGGCTAACTCTG 494

DB 421 CATTAACCTAATACCTTATGTTGTTTGAAGCTTACCGACAAATGAAGCAACCGGCTAACTCTG 480
QY 495 TGCGACAGCCCGGTAATACAGAGGTGCAAGCCTTAATGCAATTAATGAGGAGTAAG 554
DB 481 TGCGACAGCCCGGTAATACAGAGGTGCAAGCCTTAATGCAATTAATGAGGAGTAAG 540
QY 555 CCGCGCTAGGCTGTTGTTTAAGTTGATGTAATCCCGGCTTCAACCTGGAACTGCA 614
DB 541 CCGCGCTAGGCTGTTGTTTAAGTTGATGTAATCCCGGCTTCAACCTGGAACTGCA 600
QY 615 TTCAAACTGCACTAGATAGTGTAGAGGCTGTGTAATTCCTGTAGAGGCTGAA 674
DB 601 TTCAAACTGCACTAGATAGTGTAGAGGCTGTGTAATTCCTGTAGAGGCTGAA 660
QY 675 ATGCGTAGATATAGAGAGAACCAAGTGGCGAAGGCGACCACTGCACTAATACGACA 734
DB 661 ATGCGTAGATATAGAGAGAACCAAGTGGCGAAGGCGACCACTGCACTGATACGACA 720
QY 735 CTGAGGTGAGAAAGGCTGGGAGCAACAGGATTAGATACCTGTPAGTCCAGCGCTAA 794
DB 721 CTGAGGTGAGAAAGGCTGGGAGCAACAGGATTAGATACCTGTPAGTCCAGCGCTAA 780
QY 795 ACGATGTCAACTACCGCTTGAAGCCTTGAAGCTTTTATGTGGCGAGCTTAACGCACTTAAGT 854
DB 781 ACGATGTCAACTACCGCTTGAAGCCTTGAAGCTTTTATGTGGCGAGCTTAACGCACTTAAGT 840
QY 855 TGACCGCTGCGGGAGTACCGCGCGCAAGGTTAAACCAATGAATTTGACGGGGGCCGCCA 914
DB 841 TGACCGCTGCGGGAGTACCGCGCGCAAGGTTAAACCAATGAATTTGACGGGGGCCGCCA 900
QY 915 CAAGCGGTGAGCATGTGTTTAAATTCGAAGCAACCGCAAGAACTTACCAAGCCTTAGC 974
DB 901 CAAGCGGTGAGCATGTGTTTAAATTCGAAGCAACCGCAAGAACTTACCAAGCCTTAGC 960
QY 975 ATCCATGAACCTTTCAAGATAGATGTGGGCTTGGGAAACATTTGAGAGAGAGTGTCTCA 1034
DB 961 ATCCATGAACCTTTCAAGATAGATGTGGGCTTGGGAAACATTTGAGAGAGAGTGTCTCA 1020
QY 1035 TGCGTGTCTGACGCTGCTGTGTGAATGTAAG 1068
DB 1021 TGCGTGTCTGACGCTGCTGTGTGAATGTTGGG 1054

RESULT 7
US-09-821-016-5
; Sequence 5, Application US/09821016
; Patent No. US2001004692A1
; GENERAL INFORMATION:
; APPLICANT: CANON INC.
; TITLE OF INVENTION: Polyhydroxyalkanoate Synthase and Gene Encoding the Same Enzym
; FILE REFERENCE: 4051021
; CURRENT APPLICATION NUMBER: US/09/821,016
; CURRENT FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Microsoft Word
; SEQ ID NO: 5
; LENGTH: 1501
; TYPE: DNA
; ORGANISM: Pseudomonas jessenii P161 ; BP-7376
US-09-821-016-5

Query Match 92.1%; Score 985.2; DB 9; Length 1501;
Best Local Similarity 95.9%; Pred. No. 1.3e-292;
Matches 1011; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 15 TGAACGCTGCGGCGGAGCCTTAACATGCAATGCAAGTCGAGCGGTAGAGAGAACTTGTCTTC 74
DB 1 TGAACGCTGCGGCGGAGCCTTAACATGCAATGCAAGTCGAGCGGTAGAGAGAACTTGTCTTC 60
QY 75 TTGAGAGCGGCGGAGCGGTGAGTAATGCTCTAGGAATCTGCTGTAAGTGGGGGATAAGCT 134
DB 61 AATTCAAGCGGCGGAGCGGTGAGTAATGCTCTAGGAATCTGCTGTAAGTGGGGGATAAGCT 120


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Db      1  TCGAGCGGTAGAGAGAGAGCTTGCTTCTCTTGAGACGCGGAGCGGCTAGATATGCTTAG 60
Qy      107 GAATCTGCTCGGTAGTGTGGGAGATTAAGCTTGGAAAACGACTTAATACCGATACGTCCT 166
Db      61  GAATCTGCTCGGTAGTGTGGGAGATTAAGCTTGGAAAACGACTTAATACCGATACGTCCT 120
Qy      167 ACCGAGAGAAAGACGAGGACCTTGGGCTTGGCGTATCAGATGAGCTAGGTGCGATTAG 226
Db      121 ACCGAGAGAAAGACGAGGACCTTGGGCTTGGCGTATCAGATGAGCTAGGTGCGATTAG 180
Qy      227 CTGTGTGTGAGGTATGTGCTACCAAGGCGATCCGTTAATCTGCAATTTTGAAGCTTA 286
Db      181 CTGTGTGTGAGGTATGTGCTACCAAGGCGATCCGTTAATCTGCTGAGAGATGAT 240
Qy      287 CAGTCACTGTAACCTGAGACACGCTGACAGCTCCCTAAGGAGGACGAGGAGGAAATAT 346
Db      241 CAGTCACTGTAACCTGAGACACGCTGACAGCTCCCTAAGGAGGACGAGGAGGAAATAT 300
Qy      347 TGGACATGTGGGCGAAGCTTGAATCCAGCCATGCGCGTGTGTGAAGAAAGTCTTGGATT 406
Db      301 TGGACATGTGGGCGAAGCTTGAATCCAGCCATGCGCGTGTGTGAAGAAAGTCTTGGATT 360
Qy      407 GTAAGACCTTAAAGTTGGAGAGAGGCTGTGAATTAATATCTGCAATTTTGAAGCTTA 466
Db      361 GTAAGACCTTAAAGTTGGAGAGAGGCTGTGAATTAATATCTGCAATTTTGAAGCTTA 420
Qy      467 CCGACAGAAATAGCACCGGCTAACTCTGTGACAGACGCGGTAATACAGAGGCTGCAA 526
Db      421 CCGACAGAAATAGCACCGGCTAACTCTGTGACAGACGCGGTAATACAGAGGCTGCAA 480
Qy      527 GCGTAACTGGAATTAATCTGGGCTAAAGGCGCGTAAAGTGTGTTTAACTGATGTA 586
Db      481 GCGTAACTGGAATTAATCTGGGCTAAAGGCGCGTAAAGTGTGTTTAACTGATGTA 540
Qy      587 AATCCCCGGGCTCAACCTGAGAACTGCAATTCATACTGATGATAGTATGATAGG 646
Db      541 AATCCCCGGGCTCAACCTGAGAACTGCAATTCATACTGATGATAGTATGATAGG 600
Qy      647 GTGTGTGAATTTCTGTGTGAGGCGTGAATGTGTGATATAGAAAGAAACCAAGTGGCG 706
Db      601 GTGTGTGAATTTCTGTGTGAGGCGTGAATGTGTGATATAGAAAGAAACCAAGTGGCG 660
Qy      707 AAGGCGACCACTGAGCTAATACTGACACTGAGGTGCGAAAGCGTGGGAGCAACAGGA 766
Db      661 AAGGCGACCACTGAGCTAATACTGACACTGAGGTGCGAAAGCGTGGGAGCAACAGGA 720
Qy      767 TTGATACCTCTGTGTGATCCAGCCGTAACGATGTCATCTAGCGTTGGAAACCTTGAAGC 826
Db      721 TTGATACCTCTGTGTGATCCAGCCGTAACGATGTCATCTAGCGTTGGGAGCTTGAAGC 780
Qy      827 TTTTATGCGCGAGCTAAGCATTAAGTTGACCGGCTGGGAGTACGCGCGCAAGCTTAA 886
Db      781 TCTTATGCGCGAGCTAAGCATTAAGTTGACCGGCTGGGAGTACGCGCGCAAGCTTAA 840
Qy      887 AACTCAAATGAATTGACGCGGCGCCGCAACAGCGGTGAGCATGTGTTTAAITCGAAGC 946
Db      841 AACTCAAATGAATTGACGCGGCGCCGCAACAGCGGTGAGCATGTGTTTAAITCGAAGC 900
Qy      947 AACGCGAAGACCTTACCAAGGCTTGAATCCATCAATGAATTTTGAAGATGATGTC 1006
Db      901 AACGCGAAGACCTTACCAAGGCTTGAATCCATCAATGAATTTTGAAGATGATGTC 960
Qy      1007 CTTTGGGAAACATTGAGACAGGTGTGTCATGTGCTGTCACTGTGTGTGAATGTAA 1066
Db      961 CTTTGGGAAACATTGAGACAGGTGTGTCATGTGCTGTCACTGTGTGTGAATGTAA 1020
Qy      1067 GG 1068
Db      1021 GG 1022

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RESULT 5

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US-09-791-592-1
; Sequence 1: Application US/09791592
; Patent No. US20010021223A1
; GENERAL INFORMATION:
; APPLICANT: Canon Inc.
; TITLE OF INVENTION: Polymethoxyalkanoate containing 3-hydroxybenzoalkanoic acid
; FILE REFERENCE: 4396021
; CURRENT APPLICATION NUMBER: US/09/791,592
; NUMBER OF SEQ ID NOS: 1
; SEQ ID NO 1
; LENGTH: 1501
; TYPE: DNA
; ORGANISM: Pseudomonas jesseni 161 strain.
US-09-791-592-1

Query Match      92.1%; Score 985.2; DB 9; Length 1501;
Best Local Similarity 95.9%; Pred. No. 1.3e-292;
Matches 1011; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

Qy      15  TGAAGCTGCGCGAGCGCTTAACATGCAAGTGCAGCGGTAGAGAAAGCTTGTCTTC 74
Db      1  TGAAGCTGCGCGAGCGCTTAACATGCAAGTGCAGCGGTAGAGAAAGCTTGTCTTC 60
Qy      75  TTGAGAGCGCGGAGCGGCTGATATGCTTGAATCTGCTGTGTGTGTGTGTGTGTGT 134
Db      61  AATTCAGCGCGGAGCGGCTGATATGCTTGAATCTGCTGTGTGTGTGTGTGTGTGT 120
Qy      135  TCGGAAAGGAGCGGCTTAATACCGCATACGCTCTAGGAGAGAAACAGGAGGACCTTGGGCGC 194
Db      121  CTCGAAAGGAGCGGCTTAATACCGCATACGCTCTAGGAGAGAAACAGGAGGACCTTGGGCGC 180
Qy      195  TTGCGCTATCAGATGAGCGCTTGAATGCTGATGATGATGATGATGATGATGATGATGAT 254
Db      181  TTGCGCTATCAGATGAGCGCTTGAATGCTGATGATGATGATGATGATGATGATGATGAT 240
Qy      255  GCGAGATACCGCTTAATGCTGTGAGAGATGATGATGATGATGATGATGATGATGATGATGAT 314
Db      241  GCGAGATACCGCTTAATGCTGTGAGAGATGATGATGATGATGATGATGATGATGATGATGAT 300
Qy      315  AGACTCTTACGCGAGCGAGCGAGTGGGGAATTTTGAACATGAGCGGAAAGCTTATCCAG 374
Db      301  AGACTCTTACGCGAGCGAGCGAGTGGGGAATTTTGAACATGAGCGGAAAGCTTATCCAG 360
Qy      375  CATGCGCGGTGTGAGAAAGCTCTTGGGCTTGAAGCACTTAACTTGGGAGAAAGG 434
Db      361  CATGCGCGGTGTGAGAAAGCTCTTGGGCTTGAAGCACTTAACTTGGGAGAAAGG 420
Qy      435  TTGTGATTAATACCTGCAATTTTGAAGTGTACGAGATTAAGCAACCGGCTTAACCTGTG 494
Db      421  CATTAACCTTAATACCTGATAGGTTTGAAGTGTACGAGATTAAGCAACCGGCTTAACCTGTG 480
Qy      495  TGCAGACGCGCGGCTTAATACAGAGGTGTGAAGCGTTAATCGGAATTAATCTGGCGTAAG 554
Db      481  TGCAGACGCGCGGCTTAATACAGAGGTGTGAAGCGTTAATCGGAATTAATCTGGCGTAAG 540
Qy      555  CGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 614
Db      541  CGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600
Qy      615  TTCAAACCTGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 674
Db      601  TTCAAACCTGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
Qy      675  ATGCGTGAATTTAGAGAGAAACCACTGTGCGAAGGCGACCACTGTGATTAATGATGATGAT 734
Db      661  ATGCGTGAATTTAGAGAGAAACCACTGTGCGAAGGCGACCACTGTGATTAATGATGATGAT 720
Qy      735  CTGAGGTGCGAAAGCGTGGGAGCAACAGATTTAATACCTGTGATGATGATGATGATGATGAT 794
Db      721  CTGAGGTGCGAAAGCGTGGGAGCAACAGATTTAATACCTGTGATGATGATGATGATGATGAT 780

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QY 843 AACGATTAGTGAACCGCTGGGAGTACCGCCGCAAGTTAAACTCAATGAATTGA 902
DB 851 AACGATTAGTGAACCGCTGGGAGTACCGCCGCAAGTTAAACTCAATGAATTGA 910
QY 903 CGGGGGCCCGCACAAAGCGGTGAGCATGTGTTTAATTCGAAGCAACCGCAAGAACTTTA 962
DB 911 CGGGGGCCCGCACAAAGCGGTGAGCATGTGTTTAATTCGAAGCAACCGCAAGAACTTTA 970
QY 963 CGAGCCTTGACATTCATTAATTTCTGAGATGATTTGGCTTCGGGAACTTGA 1022
DB 971 CGAGCCTTGACATTCATTAATTTCTGAGATGATTTGGCTTCGGGAACTTGA 1030
QY 1023 ACAGGTGCTGATGCTGTGCTGAGCTGCTGTGTTGAAATGTAAAG 1068
DB 1031 ACAGGTGCTGATGCTGTGCTGAGCTGCTGTGTTGAAATGTAAAG 1076

RESULT 3
US-10-007-527A-12
; Sequence 12, Application US/10007527A
; Publication No. US20030044807A1
; GENERAL INFORMATION:
; APPLICANT: Tomb, Jean-Francois
; APPLICANT: Bramucci, Michael G.
; APPLICANT: Cheng, Qiong
; APPLICANT: Kostichka, Kristy N.
; TITLE OF INVENTION: Rhodococcus Cloning and Expression Vectors
; FILE REFERENCE: CL1709 US NA
; CURRENT APPLICATION NUMBER: US/10/007,527A
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: 60/254,868
; PRIOR FILING DATE: 2000-12-12
; SOFTWARE: Microsoft Office 97
; SEQ ID NO: 12
; LENGTH: 1424
; TYPE: DNA
; ORGANISM: Rhodococcus AN12
US-10-007-527A-12

Query Match 92.5%; Score 990; DB 15; Length 1424;
Best Local Similarity 98.0%; Pred. No. 4.1e-294;
Matches 1002; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 47 TCGAGCGCTAGAGAGAACTTCTCTCTTGAAGAGCGGAGCGGTGATTAATGCTTGA 106
DB 1 TCGAGCGCTAGAGAGAACTTCTCTCTTGAAGAGCGGAGCGGTGATTAATGCTTGA 60
QY 107 GAATCTGCTGTAGTGGGAGATTAAGCTTCGAAACGAGCGCTTAATACCGCATAGCTCT 166
DB 61 GAATCTGCTGTAGTGGGAGATTAAGCTTCGAAACGAGCGCTTAATACCGCATAGCTCT 120
QY 167 ACAGGAAAGACAGGGAACTTGGGCTTGGCTTATCGATGAGCTTGGCTGATTTAG 226
DB 121 ACAGGAAAGACAGGGAACTTGGGCTTGGCTTATCGATGAGCTTGGCTGATTTAG 180
QY 227 CTAGTGTGATTAATGCTTCAACAGGCGAGCATCCCTTAATGCTGTGAGAGATGAT 286
DB 181 CTAGTGTGATTAATGCTTCAACAGGCGAGCATCCCTTAATGCTGTGAGAGATGAT 240
QY 287 CAGTCACTGGAACCTGAGACAGGTTCAGACTCTTAACGGGAGCGAGCTGGGAAATAT 346
DB 241 CAGTCACTGGAACCTGAGACAGGTTCAGACTCTTAACGGGAGCGAGCTGGGAAATAT 300
QY 347 TGGACATGGGCGAAAGCTGATCCAGCATGCGCGGTGTGAGAAAGCTTTGCGATTT 406
DB 301 TGGACATGGGCGAAAGCTGATCCAGCATGCGCGGTGTGAGAAAGCTTTGCGATTT 360
QY 407 GTAAAGCACTTTAAGTTGGAGAGAGGTTGATTAATCTCTGCAATTTTGAAGTTA 466
DB 361 GTAAAGCACTTTAAGTTGGAGAGAGGTTGATTAATCTCTGCAATTTTGAAGTTA 420

QY 467 CCGACAGATTAAGACACCGGCTACTCTGAGCAGACGCGGTTAATACAGAGGTCGAA 526
DB 421 CCGACAGATTAAGACACCGGCTACTCTGAGCAGACGCGGTTAATACAGAGGTCGAA 480
QY 527 GCGTTAATCGAATTAATGAGCGGTAAACGCGCGGTGAGTTGTTAAGTTGAATGGA 586
DB 481 GCGTTAATCGAATTAATGAGCGGTAAACGCGCGGTGAGTTGTTAAGTTGAATGGA 540
QY 587 AATCCCGGAGCTCAACCTGGGAACTGCAATTCATTAATCTGATGATGATGATGAG 646
DB 541 AATCCCGGAGCTCAACCTGGGAACTGCAATTCATTAATCTGATGATGATGATGAG 600
QY 647 GTGTTGAATTTCTGTGTGAGCGGTAAATGCGTATGATTAAGAAAGAAACCAAGTGG 706
DB 601 GTGTTGAATTTCTGTGTGAGCGGTAAATGCGTATGATTAAGAAAGAAACCAAGTGG 660
QY 707 AAGGCGACCACTGACCTAATCTGACATGAGGTGCGAAAGCGTGGGAGCAACAGGA 766
DB 661 AAGGCGACCACTGACCTAATCTGACATGAGGTGCGAAAGCGTGGGAGCAACAGGA 720
QY 767 TTGATTAACCTGCTGATGCTCCAGCGCTTAAACGATGCACTAGCGTTGAAAGCTTGA 826
DB 721 TTGATTAACCTGCTGATGCTCCAGCGCTTAAACGATGCACTAGCGTTGAAAGCTTGA 780
QY 827 TTTTATGCGCGCACTTAAGCATTTAAGTTGACCGCTTGGGAGTACCGCCGCAAGTTAA 886
DB 781 TTTTATGCGCGCACTTAAGCATTTAAGTTGACCGCTTGGGAGTACCGCCGCAAGTTAA 840
QY 887 AACTCAATGAATTAAGAGCGGCGCGCAACAGCGGTGAGATGTTTAAATCGAAGC 946
DB 841 AACTCAATGAATTAAGAGCGGCGCGCAACAGCGGTGAGATGTTTAAATCGAAGC 900
QY 947 AACGCGAAGACCTTAACAGGCTTGAATCAATCAATCAATCTTCTAGACATGATTTGTC 1006
DB 901 AACGCGAAGACCTTAACAGGCTTGAATCAATCAATCAATCTTCTAGACATGATTTGTC 960
QY 1007 CTTGCGGAACTTGAAGACAGGTGCTGATGCTGCGACGCTGCTGTTGAAATGTA 1066
DB 961 CTTGCGGAACTTGAAGACAGGTGCTGATGCTGCGACGCTGCTGTTGAAATGTA 1020
QY 1067 GG 1068
DB 1021 GG 1022

RESULT 4
US-10-007-452-12
; Sequence 12, Application US/10007452
; Publication No. US20030093701A1
; GENERAL INFORMATION:
; APPLICANT: Tomb, Jean-Francois
; APPLICANT: Bramucci, Michael G.
; APPLICANT: Cheng, Qiong
; APPLICANT: Kostichka, Kristy N.
; TITLE OF INVENTION: Rhodococcus Cloning and Expression Vectors
; FILE REFERENCE: CL1709 US NA
; CURRENT APPLICATION NUMBER: US/10/007,452
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: 60/254,868
; PRIOR FILING DATE: 2000-12-12
; SOFTWARE: Microsoft Office 97
; SEQ ID NO: 12
; LENGTH: 1424
; TYPE: DNA
; ORGANISM: Rhodococcus AN12
US-10-007-452-12

Query Match 92.5%; Score 990; DB 15; Length 1424;
Best Local Similarity 98.0%; Pred. No. 4.1e-294;
Matches 1002; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 47 TCGAGCGCTAGAGAGAACTTCTCTCTTGAAGAGCGGAGCGGTGATTAATGCTTGA 106

Db 121 GTGGGGGATTAAGGTTGGAAACGACGCTAATACCGCATACGCTCTACGGGAGAAACAG 180
QY 181 GGACCTTCGGGCTTGGCGCTATCATAGATGAGCGCTAGCTAGCTAGCTAGCTAGCTAGCT 240
Db 181 GGACCTTCGGGCTTGGCGCTATCATAGATGAGCGCTAGCTAGCTAGCTAGCTAGCTAGCT 240
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Db 241 AATGCTCAACGAGCGAGCATCCGTAATCTGCTGAGAGAGATGATCACTCACTGAAA 300
QY 301 CTGAGACACGCTCCAGACTCTTAACGAGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAG 360
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QY 361 AAGCTGATCCAGCCATGCGCGCTGTGTGAAGAGGTTCTGGAATGTTAAAGCACTTTAA 420
Db 361 AAGCTGATCCAGCCATGCGCGCTGTGTGAAGAGGTTCTGGAATGTTAAAGCACTTTAA 420
QY 421 GTTGGGAGGAGGTTGTAGATTATACCTGAGCAATTTGACGTTACCGACAGATAGC 480
Db 421 GTTGGGAGGAGGTTGTAGATTATACCTGAGCAATTTGACGTTACCGACAGATAGC 480
QY 481 ACCGCTTAATCTGTGCGACGACGCGCGGTAAATACAGAGGTTGCAAGCGTTAATCGGAT 540
Db 481 ACCGCTTAATCTGTGCGACGACGCGCGGTAAATACAGAGGTTGCAAGCGTTAATCGGAT 540
QY 541 TACTGGGCTTAAGGCGCGGTAGTGTGTTTGTAGTGTGATGTGAATCCCGGGCTCA 600
Db 541 TACTGGGCTTAAGGCGCGGTAGTGTGTTTGTAGTGTGATGTGAATCCCGGGCTCA 600
QY 601 ACCGCGGAACTGCTATTCATAAAGTGAAGTGTAGAGGTTGAGGTTGGAATTTCC 660
Db 601 ACCGCGGAACTGCTATTCATAAAGTGAAGTGTAGAGGTTGAGGTTGGAATTTCC 660
QY 661 TGTGTAGCGGTAAATGCGTATATATAGAAAGAAACACAGTGGCGAAAGCGACACTG 720
Db 661 TGTGTAGCGGTAAATGCGTATATATAGAAAGAAACACAGTGGCGAAAGCGACACTG 720
QY 721 GACTAATCTGACATGAGGTGCGAAACGCTGAGGAGGAAACAGAGTTAATACCTGCT 780
Db 721 GACTAATCTGACATGAGGTGCGAAACGCTGAGGAGGAAACAGAGTTAATACCTGCT 780
QY 781 AGTCAACGCGGTAAACGATGTCAATACCGCTTGAAGCTTGAAGCTTGAAGCTTGAAG 840
Db 781 AGTCAACGCGGTAAACGATGTCAATACCGCTTGAAGCTTGAAGCTTGAAGCTTGAAG 840
QY 841 CTAAAGCATTAAGTGAACGCGCTGAGGAGTACGCGCGGAAAGTTAAATCAATGAT 900
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QY 901 GACGAGGAGCGCGCAACAGCGGTGAGCATGTGTTTAATTCGAAGCAACCGGAAGACT 960
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QY 1021 AGACAGGCTGATGAGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1070
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RESULT 2

US-09-737-297-5

Sequence 5, Application US/09737297

Patent No. US2002072108A1

GENERAL INFORMATION:

APPLICANT: Berry, Mark

APPLICANT: Griffiths, Allen

APPLICANT: Hill, Philip

APPLICANT: Laybourne-Parry, Johanna

APPLICANT: Mills, Sarah

FILE OF INVENTION: Processes and Organisms for the Production of Antifreeze Proti
FILE REFERENCE: F3347
CURRENT APPLICATION NUMBER: US/09/737,297
CURRENT FILING DATE: 2000-12-15
PRIOR APPLICATION NUMBER: GB 9929696.4
PRIOR FILING DATE: 1999-12-15
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patent in version 3.0
SEQ ID NO 5
LENGTH: 1140
TYPE: DNA
ORGANISM: Pseudomonas syzyxantha
US-09-737-297-5

Query Match 98.7%; Score 1056.4; DB 9; Length 1140;
Best Local Similarity 99.4%; Pred. No. 1.8e-314;
Matches 1060; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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11 CTGGCTCAGATTGAAGCTGGGCGGAGCGCTCAACATGCAATGCAAGCGGTAGAGAGA 70
QY 63 AGCTTGTCTCTTGAAGCGGCGGAGCGGCTGATGATGCTAGATCTGCTGCTAGT 122
Db 71 AGCTTGTCTCTTGAAGCGGCGGAGCGGCTGATGATGCTAGATCTGCTGCTAGT 130
QY 123 GGGGATTAAGCTTGGAAACGAGCGCTTAATCCGCTAGCTCTACGGAGAAACAGAG 182
Db 131 GGGGATTAAGCTTGGAAACGAGCGCTTAATCCGCTAGCTCTACGGAGAAACAGAG 190
QY 183 GACCTTGGGCGCTTGGCGCTATCAGATGAGCTGAGTATGATGATGATGATGATGAT 242
Db 191 GACCTTGGGCGCTTGGCGCTATCAGATGAGCTGAGTATGATGATGATGATGATGAT 250
QY 243 TGGCTCAACGAGCGAGATCCGTAATCTGCTGAGAGATGATGATGATGATGATGAT 302
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QY 303 GAGACAGGTCAGACTCTTACGAGGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAG 362
Db 311 GAGACAGGTCAGACTCTTACGAGGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAG 370
QY 363 GCTGATCCAGCCATGCGCGGTGTGTAGAGAGGCTTTCGATTTGAAGCACTTAAGT 422
Db 371 GCTGATCCAGCCATGCGCGGTGTGTAGAGAGGCTTTCGATTTGAAGCACTTAAGT 430
QY 423 TGGAGGAGGAGGTTGTAGATTATCTGCAATTTTGAAGTACCGAGAAATAGAGC 482
Db 431 TGGAGGAGGAGGTTGTAGATTATCTGCAATTTTGAAGTACCGAGAAATAGAGC 490
QY 483 CGGCTTAATCTGTGCGACGAGCGCGGTAAATACAGAGGTTGCAAGCGTTAATCGAATTA 542
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QY 543 CTGGGCGTAAAGCGCGGTGTGTGTTTGAAGTGTGAATGTTGTTGTTGTTGTTGTTG 602
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QY 603 CTGGGAATGATTCATAAATCTGATAGATGATGATGATGATGATGATGATGATGATGAT 662
Db 611 CTGGGAATGATTCATAAATCTGATAGATGATGATGATGATGATGATGATGATGATGAT 670
QY 663 TGTAGCGGTAAATGCTATATATAGAAAGAAACACAGTGGCGAAAGCGAGCACTGGA 722
Db 671 TGTAGCGGTAAATGCTATATATAGAAAGAAACACAGTGGCGAAAGCGAGCACTGGA 730
QY 723 CTAAATCTGACATGAGGTGCGAAAGCGTGGGAGCGAAACAGAGATTAGATCTGCTAG 782
Db 731 CTAAATCTGACATGAGGTGCGAAAGCGTGGGAGCGAAACAGAGATTAGATCTGCTAG 790
QY 783 TCCAGCGCGTAAACGATGTCAATGATGATGATGATGATGATGATGATGATGATGAT 842
Db 791 TCCAGCGCGTAAACGATGTCAATGATGATGATGATGATGATGATGATGATGATGAT 850

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OM nucleic - nucleic search, using sw model

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9593.704 Million cell updates/sec

Title: US-09-737-297-2

Perfect score: 1070

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Gapop 10.0, Gapext 1.0

Searched: 2434939 seqs, 1822278265 residues

Total number of hits satisfying chosen parameters: 4869878

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
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2	1056.4	98.7	1140	9	US-09-737-297-5
3	990	92.5	1424	15	US-10-007-527A-12
4	990	92.5	1424	15	US-10-007-452-12
5	985.2	92.1	1501	9	US-09-791-582-1
6	985.2	92.1	1501	9	US-09-745-476-1
7	985.2	92.1	1501	9	US-09-821-016-5
8	985.2	92.1	1501	9	US-09-748-205-1
9	985.2	92.1	1501	9	US-09-793-920A-1
10	985.2	92.1	1501	10	US-09-951-720A-1
11	985.2	92.1	1501	11	US-09-791-610-1
12	985.2	92.1	1501	13	US-10-242-696-1
13	985.2	92.1	1501	13	US-10-411-319-1
14	985.2	92.1	1501	15	US-10-218-519-5
15	985.2	92.1	1501	15	US-10-266-787-5

16	985.2	92.1	1501	15	US-10-252-518-5	Sequence 5, Appli
17	985.2	92.1	1501	15	US-10-105-305-1	Sequence 1, Appli
18	985.2	92.1	1501	15	US-10-133-404A-1	Sequence 1, Appli
19	907.4	84.8	1457	9	US-09-726-774-3	Sequence 3, Appli
20	856	80.0	1537	13	US-10-029-397A-46	Sequence 46, Appli
21	832.6	77.8	1481	9	US-09-737-297-4	Sequence 1, Appli
22	830.6	77.6	1486	9	US-09-737-297-1	Sequence 1, Appli
23	820.8	76.7	1506	13	US-10-278-942-1	Sequence 1, Appli
24	807	75.4	1494	14	US-10-007-725-5	Sequence 47, Appli
25	805.4	75.3	1457	13	US-10-029-397A-47	Sequence 35, Appli
26	803.8	75.1	1534	13	US-10-029-397A-35	Sequence 35, Appli
27	801	74.9	1487	9	US-09-726-774-14	Sequence 14, Appli
28	799.6	74.7	1485	13	US-10-029-397A-48	Sequence 48, Appli
29	798.8	74.7	1506	9	US-09-027-439-3	Sequence 3, Appli
30	798.4	74.6	1542	11	US-09-940-925A-158	Sequence 158, App
31	798.4	74.6	1542	11	US-09-941-132A-158	Sequence 158, App
32	798.4	74.6	1542	15	US-10-061-071-33	Sequence 33, Appli
33	798.2	74.6	1541	9	US-09-027-439-7	Sequence 7, Appli
34	798	74.6	1505	9	US-09-027-439-4	Sequence 4, Appli
35	791	73.9	1453	9	US-09-027-439-5	Sequence 5, Appli
36	791	73.9	1549	9	US-09-912-020-89	Sequence 89, Appli
37	791	73.9	1549	9	US-09-912-020-242	Sequence 242, App
38	791	73.9	1549	9	US-09-912-020-402	Sequence 402, App
39	790.2	73.9	1541	9	US-09-027-439-6	Sequence 2, Appli
40	789.4	73.8	1505	9	US-09-027-439-6	Sequence 8, Appli
41	784.4	73.3	1429	10	US-09-934-868-81	Sequence 81, Appli
42	783.8	73.3	1450	9	US-09-726-774-1	Sequence 1, Appli
43	783	73.2	1540	10	US-09-967-376-1	Sequence 1, Appli
44	783	73.2	1540	15	US-10-260-647-1	Sequence 1, Appli
45	782.6	73.1	1547	12	US-10-418-861B-53	Sequence 53, Appli

ALIGNMENTS

RESULT 1
US-09-737-297-2
Sequence 2, Application US/09737297
Patent No. US20020072108A1
GENERAL INFORMATION:
APPLICANT: Berry, Mark
APPLICANT: Griffiths, Allen
APPLICANT: Hill, Philip
APPLICANT: Laybourne-Patry, Johanna
APPLICANT: Mills, Sarah
TITLE OF INVENTION: Processes and Organisms for the Production of Antifreeze Prote
FILE REFERENCE: F3247
CURRENT APPLICATION NUMBER: US/09/737,297
PRIOR APPLICATION NUMBER: GB 9929696.4
PRIOR FILING DATE: 1999-12-15
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 1070
TYPE: DNA
ORGANISM: Pseudomonas (NCIMB 41076)
US-09-737-297-2

Query Match 100.0%; Score 1070; DB 9; Length 1070;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1070; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCCTTCTAGATGAGCGCGGCGGCTTACACATGCAATGCGGCGTAGAGA 60
DB 1 GCCCTTCTAGATGAGCGCGGCGGCTTACACATGCAATGCGGCGTAGAGA 60
QY 61 GAAGCTGCTTCTTCTGAGAGCGCGGCGGCTTATGCTAGGAATCTGCTGGTA 120
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Db 494 AAGCAGCGCTAATCTGTGTCAGACGCGCGGTAAATACAGAGGGTCAAGCGTTAATCC 553
QY 537 GAATTAATCTGGCGTAAAGCGCGGTGTGTGTTAAGTTGAATGTGAAATCCCGGG 596
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Db 614 CTCAACCTGGGAATCGATTCAAAATGACTGACTGATAGATAGTGAAGGCTGTGAAT 673
QY 657 TTCCTGTGAGCGGTGAATGCGTGAATATAGAGAAACACCAAGTGGCAAGGCGACCA 716
Db 674 TCCCGGTGTGAGCGGTGAATGCGTGAATATAGAGAAACATCTGTGGCAAGGCGGCA 733
QY 717 CTTGAGCTAATTAATCTGACACTGAGTGTGAAAGCGGTGGAGCAAAACAGATTAAGTACC 776
Db 734 TCTGAGCAGACTGACACTGAGTGTGAAAGCGGTGGAGCAAAACAGATTAAGTACC 793
QY 777 TGTGATGTCAGCGCGTAAAGCATGTCATAGCCGTGGAAAGC-CTTGAAGCTTTTATGG 835
Db 794 TGTGATGTCAGCGCGTAAAGCATGTCATAGCCGTGGAAAGC-CTTGAAGCTTTTATGG 853
QY 836 CGCAGCTTAACGCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 895
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QY 896 GAATTAAGCGGGGCGCGCAGACAGCGGTGAGCATGTGTGTTAATTAATTAATTAATTAAT 955
Db 914 GAATTAAGCGGGGCGCGCAGACAGCGGTGAGCATGTGTGTTAATTAATTAATTAATTAAT 973
QY 956 AACCTTAACAGCGCTTGAACATCAATGAATCTTCTAGAGATAGATGTGCTTGGGAA 1015
Db 974 AACCTTAACAGCGCTTGAACATCAATGAATCTTCTAGAGATAGATGTGCTTGGGAA 1033
QY 1016 CATGAGACAGGTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 1068
Db 1034 CCGTGAACAGGTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 1086

RESULT 14
US-09-602-417-1
Sequence 1, Application US/09602417
Patent No. 6326346
GENERAL INFORMATION:
APPLICANT: Brenchley, Jean E.
APPLICANT: Loveland-Curtze, Jennifer
APPLICANT: Gutshall, Kevin R.
APPLICANT: Humphrey, Vickie L.
TITLE OF INVENTION: Stain Removing Compositions Containing Particular
TITLE OF INVENTION: Isolated and Pure Proteolytic Enzymes
FILE REFERENCE: PS098-2040
CURRENT APPLICATION NUMBER: US/09/602,417
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 1449
TYPE: DNA
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: bacteria

US-09-602-417-1
Query Match 71.4%; Score 764.2; DB 4; Length 1449;
Best Local Similarity 83.8%; Pred. No. 96-260;
Matches 892; Conservative 0; Mismatches 163; Indels 9; Gaps 2;
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QY 75 TGAAGCTGGCGGAGGCTTACATGAGTGAAGTGAAGGCTGAGAGAGAGCTTCTTC 126
Db 61 CTATAGGAGGAG 120
QY 127 GATTAAGTGGAG 186
Db 121 GATTAAGTGGAG 180
QY 187 TTGCGGCTGGCGCTATGATGAGCTGATGAGCTGATGAGCTGATGAGCTGATGAGCTGAT 246
Db 181 TTGCGGCTGGCGCTATGATGAGCTGATGAGCTGATGAGCTGATGAGCTGATGAGCTGAT 240
QY 247 TCACCAAGGCGAGATCGCTAACTGCTGAGAGAGATGATGATGATGATGATGATGATGAT 306
Db 241 CCACCAAGGCGAGATCGCTAACTGCTGAGAGAGATGATGATGATGATGATGATGATGATGAT 300
QY 307 CAGGCTCCAGATCTCTTACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 366
Db 301 CAGGCTCCAGATCTCTTACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
QY 367 GATCCAGCATGCGCGGTGTGTAAGAGAGTCTTGGATTTGAAGCACTTAAGTTGGG 426
Db 361 GATCCAGCATGCGCGGTGTGTAAGAGAGTCTTGGATTTGAAGCACTTAAGTTGGG 420
QY 427 AGAAGGCTTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 486
Db 421 AGAAGGCTTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 480
QY 487 TAACTGTGCGAG 546
Db 481 TAACTGTGCGAG 540
QY 547 GCGTAAAGCGCGGTGAGTGTGTTGTTGAATGATGAAATCCCGGCTCAACTGG 606
Db 541 GCGTAAAGCGCGGTGAGTGTGTTGTTGAATGATGAAATCCCGGCTCAACTGG 600
QY 607 GAATGCTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 666
Db 601 GAATGCTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 660
QY 667 GCGTAAAGCGCGGTGAGTGTGTTGTTGAATGATGAAATCCCGGCTCAACTGG 726
Db 661 GCGTAAAGCGCGGTGAGTGTGTTGTTGAATGATGAAATCCCGGCTCAACTGG 720
QY 727 TACTGACACTGAGTGTGAG 786
Db 721 TACTGACACTGAGTGTGAG 780
QY 787 CGCGCTAAAGCATGCTAATGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 845
Db 781 CGCGCTAAAGCATGCTAATGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
QY 846 GCATTAAAGTGAACCGCTTGGAGAGTACCGCGCAAGGTTAAATCAATGAATTAAGAG 905
Db 841 GCATTAAAGTGAACCGCTTGGAGAGTACCGCGCAAGGTTAAATCAATGAATTAAGAG 900
QY 906 GGGCCCGCAGAGCGGTGAGTGTGTTAATTCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 965
Db 901 GGGCCCGCAGAGCGGTGAGTGTGTTAATTCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
QY 966 GGGCTTGAATCAATGAATCTTCTAGAGATAGTGTGCTTGGAGAGATTAAGACA 1025
Db 961 GGGCTTGAATCAATGAATCTTCTAGAGATAGTGTGCTTGGAGAGATTAAGACA 1020

APPLICANT: WALKER, Harrell L.
 APPLICANT: HIGGINBOTHAM, Lawrence R.
 TITLE OF INVENTION: CONTROL OF CYANOBACTERIA WITH A BACTERIUM
 FILE REFERENCE: 013243-0007
 CURRENT APPLICATION NUMBER: US/09/228,184
 CURRENT FILING DATE: 1999-01-11
 NUMBER OF SEQ. ID NOS: 1
 SOFTWARE: Patent Ver. 2.1
 SEQ ID NO 1
 LENGTH: 1540
 TYPE: DNA
 ORGANISM: Unknown Organism
 FEATURE:
 OTHER INFORMATION: Description of Unknown Organism: Bacterium SG-3;
 OTHER INFORMATION: gram negative, rod-shaped, exhibits flagellate
 OTHER INFORMATION: motility; pathogenic to cyanobacteria and algae;
 OTHER INFORMATION: yellow colonies on BG-11 medium suppl. with tryptic
 US-09-228-184-1

Query Match 73.2%; Score 783; DB 4; Length 1540;
 Best Local Similarity 84.4%; Pred. No. 2, Ie-266;
 Matches 906; Conservative 0; Mismatches 160; Indels 7; Gaps 2;

QY	3	CTTGTCTAGATTGAACGCTGGCGGCGAGCTTACACATGCAAGTGGAGCGGTAGAGAGA	62
DB	14	CTTGCTCAGAGTGAACGCTGGCGGCGAGCTTACACATGCAAGTGGAGCGGAGAGAGA	73
QY	63	AGCTTCTCTCTT-----GAGAGCGGCGGAGCGGTAGTAACTCTAGGAATCTGCT	116
DB	74	CAGTAGCATATCTGTGGGTGGCGAGTGGCGGAGGTAGGAATCATCGGAATCTGCTCC	133
QY	117	GATAGTGGGGGATTAAGTTCGGAACGAGCGATTAATACCGCATAGTCTTACGGGAGAA	176
DB	134	AGTCGTGGGGGATTAATAGGGGAACTTATGCTAATACCGCATAGTCTTACGGGAGAA	193
QY	177	GCAAGGGAACCTTGGGCTTGGCGCTATCATAGAGCGTAAAGTGGATTAGTGGTG	236
DB	194	GCGGGGAGATCGCAAGACCTCGCGCATGATGAGCCGATGCCATTAGTGGTGCG	253
QY	237	AGGTAAAGGCTCCCAAGGCGAGCATCCGTAATGCTGTGAGAGGATGATGATGACACT	296
DB	254	GCGTAATGCGCCCAAGGCGAGCATCCGTAATGCTGTGAGAGGATGATGATGACACT	313
QY	297	GGAATGAGACACGCTCCGACTCTTACCGGAGGAGCAGAGTGGGGAATATTGCAATGG	356
DB	314	GGAATGAGACACGCTCCGACTCTTACCGGAGGAGCAGAGTGGGGAATATTGCAATGG	373
QY	357	GCGAAAGCTGATCCAGCGCATGCCGCTGTGTGAAGAGTCTTCCGATTGTAAGCACT	416
DB	374	GCGCAAGCTGATCCAGCGCATGCCGCTGTGTGAAGAGGCTTCCGATTGTAAGCACT	433
QY	417	TTAAGTTGGAGAGAGGTTGATTAATTAATCTGCAATTTTGAAGTTCGACAGAT	476
DB	434	TTTGTCCGAAAGAAAGCATGATTAATTAATCTGCAATTTTGAAGTTCGACAGAT	493
QY	477	AAGCAACCGCTAATCTGTGCGACAGACCGCGGTAAATACAGGGTGTGAACGTTATCG	536
DB	494	AAGCAACCGCTAATCTGTGCGACAGACCGCGGTAAATACAGGGTGTGAACGTTATCG	553
QY	537	GAATTAAGGCGGTAAAGCGCGTAGTGTGTTTGAATGATGATGATGATGATGATGAT	596
DB	554	GAATTAAGGCGGTAAAGCGCGTAGTGTGTTTGAATGATGATGATGATGATGATGAT	613
QY	597	CTCAACCTGGGAACCTGATTAACAATGATGATGATGATGATGATGATGATGATGAT	656
DB	614	CTCAACCTGGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	673
QY	657	TTCTGTGTAGCGGTGAATGCGTAGATTAGAGAGAAACCAAGTGGCGAGAGCGCA	716
DB	674	TCCCGGTGTAGCGGTGAATGCGTAGAGTGGAGAGAAACATCTGTGCGAGAGCGCGCA	733
QY	717	CTGGAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	776

DB	734	TCTGACACAGACTGACACTGAGGACGAAACCGTGGGAGCAAAACAGATTAGATACC	793
QY	777	TGTAATCCAGCCGCTAAACAGATGCACTAGCCGTGGAAGC-CTTAGATTATGATG	835
DB	794	TGTAATCCAGCCCTTAACAGATGCACTAGGATGATGATGATGATGATGATGATGAT	853
QY	836	CGAGCTTAACGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT	895
DB	854	CGAGCTTAACGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT	913
QY	896	GAATTAAGGCGGCGCGGAGAGCGGTGAGCATGATGATGATGATGATGATGATGATGAT	955
DB	914	GAATTAAGGCGGCGCGGAGAGCGGTGAGCATGATGATGATGATGATGATGATGATGAT	973
QY	956	AACCTTACAGGCTTGCATCATCAATGAATCTTTAGAGATAGATGATGATGATGATGAT	1015
DB	974	AACCTTACAGGCTTGCATCATCAATGAATCTTTAGAGATAGATGATGATGATGATGAT	1033
QY	1016	CATGAGACAGGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1068
DB	1034	CGTACACAGGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1086

RESULT 13
 US-09-967-376-1
 Sequence 1, Application US/09967376
 Patent No. 6482635
 GENERAL INFORMATION:
 APPLICANT: WALKER, Harrell L.
 APPLICANT: HIGGINBOTHAM, Lawrence R.
 TITLE OF INVENTION: CONTROL OF CYANOBACTERIA WITH A BACTERIUM
 FILE REFERENCE: 013243-0007
 CURRENT APPLICATION NUMBER: US/09/967,376
 CURRENT FILING DATE: 2001-09-28
 NUMBER OF SEQ ID NOS: 1
 SOFTWARE: Patent Ver. 2.1
 SEQ ID NO 1
 LENGTH: 1540
 TYPE: DNA
 ORGANISM: Unknown Organism
 FEATURE:
 OTHER INFORMATION: Description of Unknown Organism: Bacterium SG-3; gram negative
 OTHER INFORMATION: rod-shaped; exhibits flagellate motility; pathogenic to
 OTHER INFORMATION: cyanobacteria and algae; yellow colonies on BG-11 medium suppl
 OTHER INFORMATION: with tryptic soy
 US-09-967-376-1

Query Match 73.2%; Score 783; DB 4; Length 1540;
 Best Local Similarity 84.4%; Pred. No. 2, Ie-266;
 Matches 906; Conservative 0; Mismatches 160; Indels 7; Gaps 2;

QY	3	CTTGTCTAGATTGAACGCTGGCGGCGAGCTTACACATGCAAGTGGAGCGGTAGAGAGA	62
DB	14	CTTGCTCAGAGTGAACGCTGGCGGCGAGCTTACACATGCAAGTGGAGCGGAGAGAGA	73
QY	63	AGCTTCTCTCTT-----GAGAGCGGCGGAGCGGTAGTAACTCTAGGAATCTGCT	116
DB	74	CAGTAGCATATCTGTGGGTGGCGAGTGGCGGAGGTAGGAATCATCGGAATCTGCTCC	133
QY	117	GATAGTGGGGGATTAAGTTCGGAACGAGCGCTTAATACCGCATAGCTTACGGGAGAA	176
DB	134	AGTCGTGGGGGATTAATAGGGGAACTTATGCTAATACCGCATAGCTTACGGGAGAA	193
QY	177	GCAAGGGAACCTTGGGCTTGGCGCTATCAATGAGCGCTAGTGGATTAAGTATGATGAT	236
DB	194	GCGGGGAGTCCCAAGACCTCGCGCATGATGATGATGATGATGATGATGATGATGAT	253
QY	237	AGGTAAAGGCTCCCAAGGCGAGCATCCGTAATGCTGTGAGAGGATGATGATGATGAT	296
DB	254	GCGTAATGCGCCCAAGGCGAGCATCCGTAATGCTGTGAGAGGATGATGATGATGAT	313
QY	297	GGAATGAGACACGCTCCGACTCTTACCGGAGGAGCAGCACTGGGGAATATTGCAATGG	356

Db 799 GGTACTCCAGCCNCTCAACATGAACTAGCTGTTGGGA-AGTCCCTTCTTAGTAGCG 857
Qy 838 CAGTACGACATTAAAGTTGACCGCTG333AGTACGCGCCGAAGTTAAACTCAATGA 897
Db 858 AAGTACGCGTTAAGTTCTCCGCTGGGGAGTACGCGCCGAAGTTAAACTCAAGAA 917
Qy 898 ATTACGCGGGGCGCGCAAGCGGTGAGACATGTGTTAATTGAAAGCAAGCGGAGAA 957
Db 918 ATTACGCGGGGCGCGCAAGCGGTGAGACATGTGTTAATTGAGTGAACGCGAAGAA 977
Qy 958 CTTACGAGCGCTTGACATCCATGAATTTCTAGAGATGATGTGTCCTTGCGGAGAA 1017
Db 978 CTTACCTACCTTGACATCTCTCGAATTTGTCAGAGATGATTTGTGCTTGCGGAGAA 1037
Qy 1018 TTGAGACAGGTGCTGACAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1068
Db 1038 GAGTACAGGTGCTGACAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1088

RESULT 11

US-08-114-695A-1
Sequence 1, Application US/08114695A
Patent No. 5508193
GENERAL INFORMATION:
APPLICANT: Mandelbaum, Raphael T.
APPLICANT: Wackelt, Lawrence P.
TITLE OF INVENTION: DEGRADATION OF S-TRIAZINES IN SOIL AND
TITLE OF INVENTION: WATER
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESS: SCHWEGMAN, LUNDBERG & MOESSNER, P. A.
STREET: 3500 IDS CENTER
CITY: MINNEAPOLIS
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/114,695A
FILING DATE: 31-AUG-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MUELLING, ANN M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 600,268US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-0331
TELEFAX: 612-339-3061
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1542 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: rRNA
ORIGINAL SOURCE:
ORGANISM: Escherichia coli
US-08-114-695A-1

Query Match 73.7%; Score 788.6; DB 1; Length 1542;
Beet Local Similarity 68.2%; Pred. No. 2.2e-268;
Matches 732; Conservative 184; Mismatches 149; Indels 8; Gaps 3;

Qy 3 CCTTCTCAGATTGAAGCTGCTGCGGCGGCTTAACACATCAAGTGAAGCGGGA-----GA 58
Db 18 CAUGGCUCAAGUUAAGCGGCGGCGGCTTAACACATCAAGUUAAGCGGGAACGGAACGCG 77
Qy 59 GAGAGCTGCTCTCT---CTTGAAGCGGCGGAGCGGAGTGAATGCTTGAAGATCTGCGC 115

Db 78 AAGAGCTUCCTUCCTUCCTUCCTUCCTUCCTUCCTUCCTUCCTUCCTUCCTUCCTUCCT 137
Qy 116 TGTAGTGGGAGATTAACGTTTCGAAACGACGCTTAATACCGATACGTTCTTACGAGAGA 175
Db 138 UGAGUAGGAGGAGUUAACUACUGGAAACGAGUUAUACCGAUAUACGUC -GCAAGCCAA 196
Qy 176 AGCAGGGGACCTTCGCGGCTTGGGCTATCAGATGAGCTTAAGTGGATTAAGTGTGT 235
Db 197 AGAGGGGACCTTCGCGGCTTGGGCTATCAGATGAGCTTAAGTGGATTAAGTGTGT 256
Qy 236 GAGCTAATGAGCTACACAGGCGACGATCCGTAATGCTGAGAGATGATGATGATGATGAT 295
Db 257 GGGUUAACGCTUACCUAGGCGACGACUCCUAGCTUGUUGUAGAGUUAACAGCGACAC 316
Qy 296 TGAAGTGAACACGCTTCCAGACTCTTACGAGGAGGACGAGTGGGGAATATTGAACAAT 355
Db 317 UGGAACUAGACACGAGUCCAGACUCCUAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 376
Qy 356 GCGGAAAGCTGATCCAGGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 415
Db 377 GCGGAAAGCTGATCCAGGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 436
Qy 416 TTTAAGTGGAGGAAAGGCTTGAATTAATCTGCAATTTGACCTTACCGACAGAA 475
Db 437 UUCACAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 496
Qy 476 TAAGACCGGCTAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 535
Db 497 GAGACCGGCTAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 556
Qy 536 GGAATTAAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 595
Db 557 GGAUUAACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 616
Qy 596 GCTCACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 655
Db 617 GCUCAACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 676
Qy 656 TTCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 715
Db 677 UUCAGAGUUAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 736
Qy 716 ACCTGATTAATCTGACACTGAGTGCAGAAAGCGTGGGAGCAACAGAGTTAGATACC 775
Db 737 CCUGAGCGAAGACUAGACGUCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 796
Qy 776 CTGCTGATCCAGCGGCTTAACGATGCACTGAGCGGTTGAGAGCCTTGAAGCTTTAGTGG 835
Db 797 CUGGAGUCCAGCGGCTTAACGATGCACTGAGCGGTTGAGAGCCTTGAAGCTTTAGTGG 856
Qy 836 CGAGCTTAACGATTAAGTTGACCGCTGAGGAGTACGCGCCGAAGTTAAACTCAAT 895
Db 857 CGAGCTTAACGATTAAGTTGACCGCTGAGGAGTACGCGCCGAAGTTAAACTCAAT 916
Qy 896 GAATTACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 955
Db 917 GAUUGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 976
Qy 956 AACCTTAACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1015
Db 977 AACCTTAACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1036
Qy 1016 GATTGAGACAGGTGCTGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1068
Db 1037 CCUGAGACAGGTGCTGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1088

RESULT 12

US-09-288-184-1
Sequence 1, Application US/09228184
Patent No. 6322782
GENERAL INFORMATION:

QY	420	AGTTGGAGAGAGAGGGTGTGATTTAAATCTCTGCATTTTGAAGTTACCGACAGATAAG	479
Db	435	AGUGGAGAGAGAGGCGAGUAAAGUAAUACUUCUCUNUUVUUGACGUUACCAACAGAAUAG	494
QY	480	CACCGGCTAACTCTGTGCCAGCACAGCCGCGTAAACAG-AGGTCGCAAGCTTAAATCGGA	538
Db	495	CACCGGCUAACUCUCGUCGACAGACCGCGGUAAUACUGAAGGUCUAGCGUUAUCCGA	554
QY	539	ATTACTGAGGCGTAAAGAGCGCGTAGTGGTTTAAAGTTGATGTGAATGCCGGGCT	598
Db	555	AUUAUCUGGGTGUAAAGCGCGCGUAGGUGUUUGUAAAGUAGUAGUAAUCCCCGGGCTU	614
QY	599	CAACCTGGGAACTTGCAATTCAAACTGACTGACTGAATAGTAGAGGAGGTGTGAATTT	658
Db	615	CAACCTGGGAGCTGCAUCCAAUACUUCUGACTGAGGAGCGUAGAGGUGUGGAUUVU	674
QY	659	CCGTGTAGGCGGTAAATGCGTTGATATAGTAAAGAAACACACAGTGGCGGAAGCGACACC	718
Db	675	CCUUGUAGCGGUGAAUUGCGUAGUAAUAGAAAGAAACACAGGUGCGAAGCGACACC	734
QY	719	TGAGCTAATACTGACACTGAGAGTGCAGAAAGCGTGGGAGCAAAACAGATTGATACCTTG	778
Db	735	UCGACUGAUCUGAGCCUGAGGUGCGCAAGC-UGGGAGACVMAACGAGUUVUAGUCCUG	793
QY	779	GTACTCCAGCCCGTAAACGATGTCAACTGACCGCTTGGAAGCCTTAACTTTAGTGGCC	838
Db	794	GUAAUCCACGCGCUGCAACGAAUUGCGACUAGCGGUGGAGUCCUUGAGUCCUAAUUGGCGC	853
QY	839	AGCTAACGCTTAATAGTTGACCGCGCTGGGAGTAGCGGCGCAAGGTTAACTCAATGAA	898
Db	854	AG-UAAAGCGUAAAGUUGACCGCUGGGCGUACGGCGCAAGGUAUAAUCUCAAAGAU	912
QY	899	TTAGCGGGGGCCCCGACCAAGCGGTGAGCATGTGTTATTCCAGAACACGCCGAAGAC	958
Db	913	U--CAAGGGGCGCGCAACCGGUGGAGCAUUGUUAUUCGAAUAAACGCCAAGAAC	969
QY	959	CTTACCAAGGCGTTGACATCCAAATGAATCTTTAGAGATAGATTGTGCTTCGGGAACAT	1018
Db	970	CUAACCUUGGCUUAGCAUUGUCGGGAUUCUUGACAGACAGUAGCAAGGACUUCUGGGAUUG	1029
QY	1019	TGAGACAGGCTGCTGCATGGCTGTCTGCACCTGCTGTT	1057
Db	1030	GAAACAAGGUGGUGCAUUGGUGCGUACAGHUCAGUGU	1068
RESULT 10			
US-08-632-470-53			
Sequence 53: Application US/08632470			
Patent No. 5976791			
GENERAL INFORMATION:			
APPLICANT: MABIAN, CLAUDE			
APPLICANT: RAOUlt, DIDIER			
TITLE OF INVENTION: NUCLEOTIDE FRAGMENTS CAPABLE OF			
HYBRIDIZING SPECIFICALLY TO RICKETTSIA RNA OR RNA AND			
TITLE OF INVENTION: THEIR USE AS PROBES OR PRIMERS			
NUMBER OF SEQUENCES: 53			
CORRESPONDENCE ADDRESS:			
ADDRESSEE: OLIFF & BERRIDGE			
STREET: P.O. BOX 19928			
CITY: ALEXANDRIA			
STATE: VA			
COUNTRY: USA			
ZIP: 22320			
COMPUTER READABLE FORM:			
MEDIUM TYPE: Floppy disk			
COMPUTER: IBM PC compatible			
OPERATING SYSTEM: PC-DOS/MS-DOS			
SOFTWARE: Patentin Release #1.0, Version #1.30			
CURRENT APPLICATION DATA:			
APPLICATION NUMBER: US/08/632,470			
FILING DATE: 08-JUL-1996			
CLASSIFICATION: 435			

Query Match	Similarity	Score	DB	Length
Beet local	84.5%	788.6	2	1484
Matches	905	Conservative	0	Mismatches 159; Indels 7; Gaps 2
<p>ATTORNEY/AGENT INFORMATION: NAME: BERRIDGE, WILLIAM P REGISTRATION NUMBER: 30,024 REFERENCE/DOCKET NUMBER: WPB 38238 TELECOMMUNICATION INFORMATION: TELEPHONE: (703)-836-6400 TELEFAX: (703)-836-2787 INFORMATION FOR SEQ ID NO: 53: SEQUENCE CHARACTERISTICS: LENGTH: 1484 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) US-08-632-470-53</p>				
Query	4	CTTGCTCAGATTGAAAGCTGCGCGAGGCTTACACATGCAAGTCGAGCGGTAGAGACA	63	
Db	19	CTGGCTCAGATTGAAAGCTGCGCGAGGCTTACACATGCAAGTCGAGCGGTAGAGACA	78	
QY	64	GCCTTCTCTCTT-----GAGAGCGGCGGAGCTAGTAATGCTTAGAATCTGCTG	117	
Db	79	GAGACTTCT	138	
QY	118	GTAAGTGGGGGATTAACGTTGCGAAACGAGCGCTAATACCGATACGTCCTTACGGGAAAG	177	
Db	139	GTAGTGGGGGATTAACGTTGCGAAACGAGCGCTAATACCGATACGTCCTTACGGGAAAG	198	
QY	178	CAGGGGACCTTTCGGGCTTCGCTTACGATGAGCTAGCTGCGATTACCTAGTTGTA	237	
Db	199	CGGGGATCTTTCGGGCTTCGCTTACGATGAGCTAGCTGCGATTACCTAGTTGTA	258	
QY	238	GGAATAGGCTACCAAGGCGAGATCCGTACCTGCTGAGAGATGATCAGTACACTG	297	
Db	259	GGAATAGGCTTACCAAGGCGAGATCCGTACCTGCTGAGAGATGATCAGTACACTG	318	
QY	298	GAACTGAGACACGGTCCAGACTCTTACCGGAGGACGACGTGGGAAATTGGACATGGG	357	
Db	319	GAACTGAGACACGGTCCAGACTCTTACCGGAGGACGACGTGGGAAATTGGACATGGG	378	
QY	358	CGAAGCTGATTCAGCCATGCCCGGTGTGAGAAAGGCTTCGATTGTAAGCACTT	417	
Db	379	GGAAGCTGATTCAGCCATGCCCGGTGTGAGAAAGGCTTCGATTGTAAGCACTT	438	
QY	418	TAACTGAGGAAAGGTTGTAATTAATCTGCAATTTTACGTTACCGACGAATTA	477	
Db	439	TAACTGAGGAAAGGTTGTAATTAATCTGCAATTTTACGTTACCGACGAATTA	498	
QY	478	AGCAGCGGCTAATCTGTGCGAGAGCCGCGGTAAATACAGAGGTCGAACGTTATCGG	537	
Db	499	AGCAGCGGCTAATCTGTGCGAGAGCCGCGGTAAATACAGAGGTCGAACGTTATCGG	558	
QY	538	AATTAATGCGGCTAAGCGCGCTAGTGTGTTGAAGTGAATGTAATCCCGCGG	597	
Db	559	AATTAATGCGGCTAAGCGCGCTAGTGTGTTGAAGTGAATGTAATCCCGCGG	618	
QY	598	TCAACTGAGGAACTGATTTCAAACTGACTGACTAGATGATGATAGAGGTGATGAAAT	657	
Db	619	TCAACTGAGGAACTGATTTCAAACTGACTGACTAGATGATGATAGAGGTGATGAAAT	678	
QY	658	TGCTGTGATGCGGTGAATGCTGATTAATGAAAGAAACACCAAGTGGCGAAGCGACAC	717	
Db	679	TGCTGTGATGCGGTGAATGCTGATTAATGAAAGAAACACCAAGTGGCGAAGCGACAC	738	
QY	718	CTGGAATAATCTGACTGAGGTGCGAAAGCGTGGGAGCAAAACAGATTGATACCTT	777	
Db	739	CTGGAATAATCTGACTGAGGTGCGAAAGCGTGGGAGCAAAACAGATTGATACCTT	798	
QY	778	GGTAGTCCAGCGCGTAAACGATGTCAACTAGCCGTTGGAAGCGTTGAGCTTTAGTGGCG	837	

60 AAGAGCTGCTTCT--CTTGAGAGCGCGGAGCGGTGAGTAATGCTAGGAATCTGCTT 116
 78 AAGAGCTGCTTCTTCTGCTGAGAGTGGCGGAGCGGTGAGTAATGCTGAGGAATCTGCTT 117
 117 GGTAGTGGGGGATACGTTGGGAAACGAGCGCTATACCGCATACGCTCTACCGGAGAA 116
 138 GATGAGGGGGATACGTTAGGAAACGAGCGCTATACCGCATACGCTCTACCGGAGAA 117
 177 GAGGAGGAGCTTCTGCGCTTCTGCTATGAGTGAAGCTGAGTGGATGAGTGGT 236
 198 GAGGAGGAGCTTCTGCGCTTCTGCTATGAGTGAAGCTGAGTGGATGAGTGGT 257
 237 AGGTATGAGCTACCAAGGAGCGAGTCCGTAAGCTGAGTGGAGGAGTACGATCCACT 296
 258 GGTATGAGCTTCTGAGCGAGCGAGTCCGTAAGCTGAGTGGAGGAGTACGATCCACT 317
 297 GAGAGTGAAGAGCGGTCCAGACTCTCTACGAGGAGCGAGTGGGGAATTTGAGCAATG 356
 318 GAGAGTGAAGAGCGGTCCAGACTCTCTACGAGGAGCGAGTGGGGAATTTGAGCAATG 377
 357 GCGAAGCTGATCCAGGAGTCCGCTGAGTGAAGAGTCTTGGATTTGAGCAATG 416
 378 GCGAAGCTGATCCAGGAGTCCGCTGAGTGAAGAGTCTTGGATTTGAGCAATG 437
 417 TTAGTGGAGAGGAGTGGTGAATTAATCTGCAATTTTGAAGCTTACCGAGCAAT 476
 438 TTAGTGGAGAGGAGTGGTGAATTAATCTTCTGCAATTTTGAAGCTTACCGAGCAAT 497
 477 AAGAGCTGAGTCTTCTGCTGAGAGCGCGGTGAATTAAGAGGAGTGAAGCTTATG 536
 498 AAGAGCTGAGTCTTCTGCTGAGAGCGCGGTGAATTAAGAGGAGTGAAGCTTATG 557
 537 GAATTAAGTGGAGTGAAGCGCGGTGAGTGGTGAATTAAGAGGAGTGAAGCTTATG 596
 558 GAATTAAGTGGAGTGAAGCGCGGTGAGTGGTGAATTAAGAGGAGTGAAGCTTATG 617
 597 CTCAAGCTGAGTGAAGCGCGGTGAGTGGTGAATTAAGAGGAGTGAAGCTTATG 656
 618 CTCAAGCTGAGTGAAGCGCGGTGAGTGGTGAATTAAGAGGAGTGAAGCTTATG 677
 657 TTCTGAGTGAAGTGAAGCGCGGTGAGTGGTGAATTAAGAGGAGTGAAGCTTATG 716
 678 TTCTGAGTGAAGTGAAGCGCGGTGAGTGGTGAATTAAGAGGAGTGAAGCTTATG 737
 717 CTGAGTGAAGTGAAGCGCGGTGAGTGGTGAATTAAGAGGAGTGAAGCTTATG 776
 738 CTGAGTGAAGTGAAGCGCGGTGAGTGGTGAATTAAGAGGAGTGAAGCTTATG 797
 777 TGTAGTGAAGTGAAGCGCGGTGAGTGGTGAATTAAGAGGAGTGAAGCTTATG 836
 798 TGTAGTGAAGTGAAGCGCGGTGAGTGGTGAATTAAGAGGAGTGAAGCTTATG 857
 837 GAGTGAAGTGAAGCGCGGTGAGTGGTGAATTAAGAGGAGTGAAGCTTATG 896
 858 GAGTGAAGTGAAGCGCGGTGAGTGGTGAATTAAGAGGAGTGAAGCTTATG 917
 897 AATTGAGGAGGAGCGCGGTGAGTGGTGAATTAAGAGGAGTGAAGCTTATG 956
 918 AATTGAGGAGGAGCGCGGTGAGTGGTGAATTAAGAGGAGTGAAGCTTATG 977
 957 AATTGAGGAGGAGCGCGGTGAGTGGTGAATTAAGAGGAGTGAAGCTTATG 1016
 978 AATTGAGGAGGAGCGCGGTGAGTGGTGAATTAAGAGGAGTGAAGCTTATG 1037
 1017 AATTGAGGAGGAGCGCGGTGAGTGGTGAATTAAGAGGAGTGAAGCTTATG 1068
 1038 CGTGAAGGAGGAGCGCGGTGAGTGGTGAATTAAGAGGAGTGAAGCTTATG 1089

RESULT 9
 US-08-114-695A-2
 Sequence 2, Application US/08114695A

Patent No. 5508193
 GENERAL INFORMATION:
 APPLICANT: Mandelbaum, Raphael T.
 APPLICANT: Wacker, Lawrence P.
 TITLE OF INVENTION: DEGRADATION OF S-TRIAZINES IN SOIL AND
 TITLE OF INVENTION: WATER
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SCHWEMAN, LUNDBERG & WOESSNER, P.A.
 STREET: 3500 IDS CENTER
 CITY: MINNEAPOLIS
 STATE: MN
 COUNTRY: USA
 ZIP: 55402
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/114,695A
 FILING DATE: 31-Aug-1993
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: MUELLER, ANN M.
 REGISTRATION NUMBER: 33,977
 REFERENCE/DOCKET NUMBER: 600,268US1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 612-339-0331
 TELEFAX: 612-339-3061
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1473 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: rRNA
 ORIGINAL SOURCE:
 ORGANISM: Pseudomonas sp. Atrazine-Degrading Isolate
 ORGANISM:
 US-08-114-695A-2

Query Match 74.1%; Score 793.4; DB 1; Length 1473;
 Best Local Similarity 70.0%; Pred. No. 4,3e-270;
 Matches 741; Conservative 198; Mismatches 111; Indels 9; Gaps 7;

3 CCTGCTCAGATGAAGCGTGGCGG--CAGGCTTAACATGAGCGAGCGTGAAGAG 61
 15 CAUGGCTCAHUGAUAUUGUGCGGUGAAGCTTAAACAUGCAUGCGAGCGGAUGAAG 74
 62 AAGCTTCTCTCTTGAG-AGCGGCGAGCGGTGAAGTAATGCTTGAAGATCTGCTG-T 119
 75 GAGCUCUCUCGCGGAAUUAUGCGGCGGAGUGGUAUUAUGCUGAUAUUCUGCUGGU 134
 120 AGTGGGGGATTAAGTTGCGAAACGAGCGTAAATACCGCATAGCTCTGAGGAGAAAGA 179
 135 AGUGGGGAGAAAGUUCGAAAGAGCGCUAUAACCGCAUAGUUCUCCGGAGAAAGUG 194
 180 GGGGACCTTGCGGCTTGGCTATCAGATGAGCTAGTGGATTAAGTACTTGGTGAAG 239
 195 GGGGUAUUCUGGAGCUCUACGCUUCCSAUGAGCUGAGGCGGAAUUAUGUAGUGGGG 254
 240 TAAAGGCTCAACAGCGAGCGAGTCCGTATCTGTGAGAGAGTATGATCACTGGA 299
 255 UAAUGGCUACCUAAGGAGAGUCCUUAUCUGUUGAAGAGUAGUACUGUACACUGGA 314
 300 ACTGAGACAGGCTCCAGACTCTTACCGGAGGAGGAGCAAGCGGGAATATTGACAAATGGGCG 359
 315 ACUGAGACAGGCTCCAGGCTTACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 374
 360 AAGGCTGATCCAGGCTCCAGGCTTACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 419
 375 AAGGCTGATCCAGGCTCCAGGCTTACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 434

/ CURRENT FILING DATE: 1999-12-16
 / PRIOR APPLICATION NUMBER: US 09/325,601
 / PRIOR FILING DATE: 1999-06-03
 / PRIOR APPLICATION NUMBER: GB 9812196.5
 / PRIOR FILING DATE: 1998-06-05
 / PRIOR APPLICATION NUMBER: GB 9904790.4
 / PRIOR FILING DATE: 1999-03-02
 / PRIOR APPLICATION NUMBER: US 60/122,439
 / PRIOR FILING DATE: 1999-03-02
 / PRIOR APPLICATION NUMBER: US 60/088,241
 / PRIOR FILING DATE: 1998-06-05
 / NUMBER OF SEQ ID NOS: 37
 / SOFTWARE: PatentIn version 3.0
 / SEQ ID NO 2
 / LENGTH: 1542
 / TYPE: RNA
 / ORGANISM: Escherichia coli
 / US-09-465-355-2

Query Match 74.6%; Score 798.4; DB 4; Length 1542;
 Best Local Similarity 68.2%; Pred. No. 7.5e-272;
 Matches 731; Conservative 184; Mismatches 151; Indels 6; Gaps 2;

QY 3 CCTTGCTCAGATTGAACGCTGCGGCGAGGCTTAACATGCAAGTCGACGCGT--AGAG 59
 DB 18 CAUGGCUCAAGUUGAACGCGCGGCGGCUAACAUCGACGUAACGUAACAGGA 77
 QY 60 AGAAGCTTGCTCT--CTTGAAGCGGCGGAGCGGCTGATGATGCTTGAATCTGCT 116
 DB 78 AGAAGGUCUCUCUCUCUCGACGAGUCGCGGCGGUAUAGUCUGGGAACUCUCU 137
 QY 117 GGTAGTGGGAGATTAACGTTCCGAAACGACGCTTAATCCGATACGCTCTTACGGAGAAA 176
 DB 138 GATGAGGGGGAAUAUAUACUGAAACGUAAGUAUACCGUAUACGUCGAACACCAA 197
 QY 177 GCAAGGGAACCTTGCGGCTTGCGCTATCATAGATGACCTTGAATGCTTGTG 236
 DB 198 GAGGGGAGACCUUGGGGCUUCUGCAUCGAGUGUCCGAGUAGGUAUAGCUAUGUG 257
 QY 237 AGGTATGCTCCACCAAGGCGACGATCCGTAATGCTGAGAGGATGATGATGACACT 296
 DB 258 GGGUAAACGCTUACCTTAGGCGAGCAUCCUAGCUGGUCUGAGAGUACGACGACACU 317
 QY 297 GGAAGCTGAGACAGCTGCACTCTTACCGGAGGAGAGAGTGGGAAATTTGAACAATG 356
 DB 318 GGAACUGAGACACGCTCCAGACUCCUACGAGGAGGAGAGGAGGAAUAGUCACAUGG 377
 QY 357 GCGAAAGCCTGATCCAGCATGCGCGCTGTGAGAGAGTCTTCCGATTTGAAGCACT 416
 DB 378 GCGCAAGCCUAGTCAGCCAUCCGCGGUAUAGAAAGCCUUCGCGGUAUAGACU 437
 QY 417 TTAAGTTGGAGAGAGGTTGATTAATACTCGCAATTTGACGTTACCGACAGAAAT 476
 DB 438 UUCAGCGGGAGAGAGGAGUAUAGUUAUACUUGUCUACUUGACGUAUACCGCAAG 497
 QY 477 AAGCAACCGGCTAATCTGTGCAAGACGCGCGGTATACAGAGGTGCAACGCTTATCG 536
 DB 498 AAGCAACCGGCTAATCTGTGCAAGACGCGCGGTATACAGAGGTGCAACGCTTATCG 557
 QY 537 GAATTACTGGCGTAAAGCGCGCTGATGCTTGTGATGATGATGATGATGATGATGAT 596
 DB 558 GAUUAUUCUGGCGUAAAGCGACGAGGCGGUGUUAUAGUACAUUAGUAAUUCGCCGG 617
 QY 597 CTCACCTGGGAATCTGATTAATACTGATGATGATGATGATGATGATGATGATGAT 656
 DB 618 CTCACCTGGGAATCTGATTAATACTGATGATGATGATGATGATGATGATGATGAT 677
 QY 657 TTCCTGTAGCGGTGAATGCTGATATAGAGAGAAACCAAGTGGCGAGAGCGACCA 716
 DB 678 UCCAGGUGUAGCGGUAUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 737
 QY 717 CTTGACTAATATGACTGAGGTGCGAAAGCGTGGGAGCAACAGATTAATATCCC 776

DB 738 CCUGAGCAAGACUAGACGUCGAGGAGGAGCAAAACAGAUUAGAUACCC 797
 QY 777 TGGTATCCAGCGCGCTTAAGATGCAATGACCGCTTGAAGCTTGAATGAGC 836
 DB 798 UGGUAGUCCACGCGGUAUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 857
 QY 837 GCACTTAACGATTAAGTTGACCGCTGGGAGTACCGCGCAAGTTAACTCAATG 896
 DB 858 GAGCUAAACGCUUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 917
 QY 897 AATTGACGGGCGCGGCAAGCGTGGAGACGATGTTAATTGCAAGAACGCAAGA 956
 DB 918 AAUUGACGGGCGCGGCAAGCGTGGAGACGATGTTAATTGCAAGAACGCAAGA 977
 QY 957 ACCTTACGAGCCTTACATCAATGAACTTTCTAGAGATGATGATGCTTGGGAAC 1016
 DB 978 ACCUACCUAGUUCUAGACUACGAGAGUUAUAGAGUAGUAGUAGUAGUAGUAG 1037
 QY 1017 ATTGAGACAGGTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1068
 DB 1038 CGUGAGACAGGUCUGCAUGGCUUCGUCAGCUCUGUUGUAGAAUUGGGG 1089

RESULT 8
 US-08-520-946-158
 / Sequence 158, Application US/08520946
 / Patent No. 6372424
 / GENERAL INFORMATION:
 / APPLICANT: BROW, MARY ANN D.
 / APPLICANT: LYAMICHEV, VICTOR I.
 / APPLICANT: OLIVE, DAVID M.
 / TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF
 / TITLE OF INVENTION: PATHOGENS
 / NUMBER OF SEQUENCES: 160
 / CORRESPONDENCE ADDRESSES:
 / ADDRESSEE: MEDLEN & CARROLL
 / STREET: 220 MONTGOMERY STREET, SUITE 2200
 / CITY: SAN FRANCISCO
 / STATE: CALIFORNIA
 / COUNTRY: UNITED STATES OF AMERICA
 / ZIP: 94104
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: PatentIn Release #1.0, Version #1.25
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/520,946
 / FILING DATE:
 / CLASSIFICATION: 435
 / ATTORNEY/AGENT INFORMATION:
 / NAME: CARROLL, PETER G.
 / REGISTRATION NUMBER: 32,837
 / REFERENCE/DOCKET NUMBER: PORS-01756
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: (415) 705-8410
 / TELEFAX: (415) 397-8338
 / INFORMATION FOR SEQ ID NO: 158:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 1542 base pairs
 / TYPE: nucleic acid
 / STRANDEDNESS: double
 / TOPOLOGY: linear
 / MOLECULE TYPE: DNA (genomic)
 / US-08-520-946-158

Query Match 74.6%; Score 798.4; DB 4; Length 1542;
 Best Local Similarity 65.4%; Pred. No. 7.5e-272;
 Matches 915; Conservative 0; Mismatches 151; Indels 6; Gaps 2;

QY 3 CCTTGCTCAGATTGAACGCTGCGGCGGCTTAACATGCAAGTCGACGCGT--AGAG 59
 DB 18 CATGCTCAGATTGAACGCTGCGGCGGCTTAACATGCAAGTCGACGCGT--AGAG 77

[illegible]

RESULT 6
US-08-757-653-158

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1 GENERAL INFORMATION:
2 APPLICANT: Kaiser, Michael W.
3 APPLICANT: Lyamichev, Victor I.
4 APPLICANT: Lyamichev, Natasha
5 TITLE OF INVENTION: Cleavage Of Nucleic Acid Using
6 TITLE OF INVENTION: Thermostable FEN-1 Endonucleases
7 NUMBER OF SEQUENCES: 190
8 CORRESPONDENCE ADDRESS:
9 ADDRESSEE: Medlen & Carroll, LLP
10 STREET: 220 Montgomery Street, Suite 2200
11 CITY: San Francisco
12 STATE: California
13 COUNTRY: United States Of America
14 ZIP: 94104
15
16 COMPUTER READABLE FORM:
17 MEDIUM TYPE: Floppy disk
18 COMPUTER: IBM PC compatible
19 OPERATING SYSTEM: PC-DOS/MS-DOS
20 SOFTWARE: Patent in Release #1.0, Version #1.30
21 CURRENT APPLICATION DATA:
22 APPLICATION NUMBER: US/08/757,653
23 FILING DATE:
24
25 CLASSIFICATION: 435
26 ATTORNEY/AGENT INFORMATION:
27 NAME: Ingolia, Diane E.
28 REGISTRATION NUMBER: 40,027
29 REFERENCE/DOCKET NUMBER: F08S-02565
30 TELECOMMUNICATION INFORMATION:
31 TELEPHONE: (415) 705-8410
32 TELEFAX: (415) 397-8338
33 INFORMATION FOR SEQ ID NO: 158:
34 SEQUENCE CHARACTERISTICS:
35 LENGTH: 1543 base pairs
36 TYPE: nucleic acid
37 STRANDEDNESS: double
38 TOPOLOGY: linear
39 MOLECULE TYPE: DNA (genomic)
40
41 US-08-757-653-158
42
43 Query Match 74.6%; Score 798.4; DB 2; Length 1542;
44 Best local Similarity 85.4%; Pred.No.7,5e-272;
45 Matches 915; Conservative 0; Mismatches 15; Indels 6; Gaps 2
46
47 QY 3 CCTTGCTCAGATTGAACGCTGGCGGACGCTTAACACATGCACTGAGCGGT--AGAG 59
48 Db 18 CATGCGTCAGATTGAACGCTGGCGGACGCTTAACACATGCAATCGTAACAGGA 77
49
50 QY 60 AGAAGCTTCTTCT--CTTAGAGCGGCGGACGCGGTGAGTAAGCTTAGAGATTCGCC 116
51 Db 78 AGAAGCTTCTTCTTCTTCTTCTCTGACGAGTGGCGGAGGTGAGTAAGTGTGGGAAATCGCCT 137
52
53 QY 117 GGTAGTGGGGGATTAACGTTGGAAACGACGCTATAACCGCATACGTCCTACCGGGGAAA 176
54 Db 138 GATGAGGGGGGATTAACCTACTGTGAAACGGTAGCTATATCCGATATAGCTGCACAGACCAA 197

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[illegible]

Db	481	TGCACAGACCGCGGTAAATACAGAGGGTCGAAAGCGTTAATCGAAATTACTAGGGGCTTAAAG	548
Oy	555	CGCGCGTAAAGGTGGTCTTTGTTAAAGTTGAACTGTGAAATATCCCCGGGCTCAACCTGGGAATCTGA	614
Db	541	CGCGCGTAAAGGTGGTCTTTGTTAAAGTTGAACTGTGAAATATCCCCGGGCTCAACCTGGGAATCTGA	600
Oy	615	TTCAAAACTGACTGACTAGAGTATGAGTAAAGGGTGTGGAATTTCTGTAGCGGTGAA	674
Db	601	TTCAAAACTGACTGACTAGAGTATGAGTAAAGGGTGTGGAATTTCTGTAGCGGTGAA	660
Oy	675	ATGGGTGATATATGAAAGGAACAACAAGTGGCGAAGGCGACCACTGATCTAATTCGAC	734
Db	661	ATGGGTGATATATGAAAGGAACAACAAGTGGCGAAGGCGACCACTGATCTAATTCGAC	720
Oy	735	CTGAGGTGCGAAAAGCGTGGGGGCAAAACAGATTGATACCTGTAGTCCAGCGCTAA	794
Db	721	CTGAGGTGCGAAAAGCGTGGGGGCAAAACAGATTGATACCTGTAGTCCAGCGCTAA	780
Oy	795	ACGATGTCAACTGACCGGTTGGAAGCCTTGACCTTTAATGGCGAGCTAAGCATTAAT	854
Db	781	ACGATGTCAACTGACCGGTTGGAAGCCTTGACCTTTAATGGCGAGCTAAGCATTAAT	840
Oy	855	TGACCGCGTGGGGAGTACGGCCCGCAAGGTTAAACTCAAATGAATTGACGGGGCCCGCA	914
Db	841	TGACCGCGTGGGGAGTACGGCCCGCAAGGTTAAACTCAAATGAATTGACGGGGCCCGCA	900
Oy	915	CAAGCGGTGAGGATGTGGTTTAATTCGAGCAACGGGAAGAACCTTACAGAGCCTTGAC	974
Db	901	CAAGCGGTGAGGATGTGGTTTAATTCGAGCAACGGGAAGAACCTTACAGAGCCTTGAC	960
Oy	975	ATCCAAATGAACTTTCTAGAGATAGATTGGTGCCTTCGGGAACATTGAGACAGGTGTGCA	1034
Db	961	ATCCAAATGAACTTTCCAGAGATAGATTGGTGCCTTCGGGAACATTGAGACAGGTGTGCA	1020
Oy	1035	TGGCTGTGCTCAGCTCGTGTGTTGAAATGTAAAG	1068
Db	1021	TGGCTGTGCTCAGCTCGTGTGTTGAAATGTAAAG	1054
RESULT 5			
US-08-114-695A-6			
: Sequence 6, Application US/08114695A			
: Patent No. 5508193			
: GENERAL INFORMATION:			
: APPLICANT: Mandelbaum, Raphael T.			
: TITLE OF INVENTION: Lawrence P.			
: TITLE OF INVENTION: DEGRADATION OF S-TRIAZINES IN SOIL AND			
: NUMBER OF SEQUENCES: 8			
: CORRESPONDENCE ADDRESS:			
: ADDRESSEE: SCHWEGMAN, LUNDBERG & WOESSNER, P.A.			
: STREET: 3500 IDS CENTER			
: CITY: MINNEAPOLIS			
: STATE: MN			
: COUNTRY: USA			
: ZIP: 55402			
: COMPUTER READABLE FORM:			
: MEDIUM TYPE: Floppy disk			
: COMPUTER: IBM PC compatible			
: OPERATING SYSTEM: PC-DOS/MS-DOS			
: SOFTWARE: Patentin Release #1.0, Version #1.25			
: CURRENT APPLICATION DATA:			
: APPLICATION NUMBER: US/08/114,695A			
: FILING DATE: 31-AUG-1993			
: CLASSIFICATION: 435			
: ATTORNEY/AGENT INFORMATION:			
: NAME: MUELLING, ANN M.			
: REGISTRATION NUMBER: 33,977			
: REFERENCE/DOCKET NUMBER: 600.268US1			
: TELECOMMUNICATION INFORMATION:			
: TELEPHONE: 612-333-0331			
: TELEFAX: 612-339-3061			
: INFORMATION FOR SEQ ID NO: 6:			

[illegible]

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; APPLICANT: CANON INC.
; TITLE OF INVENTION: Preparation of Poly-hydroxyalkanoic Acid
; FILE REFERENCE: 4351008
; CURRENT APPLICATION NUMBER: US/09/745,476
; CURRENT FILING DATE: 2000-12-26
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Microsoft Word
; SEQ ID NO: 1
; LENGTH: 1501
; TYPE: DNA
; ORGANISM: Pseudomonas jessenii 161 ; FERM P-17445
; US-09-745-476-1

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Query Match      92.1% Score 985.2; DB 4; Length 1501;
Best Local Similarity 95.9%; Pred. No. 0;
Matches 1011; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

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QY 15 TGAACGCTGGCGGCGGCTTAACACATGCAAGTCGAGCGGTAGAGAAAGCTTGTCTC 74
DB 1 TGAACGCTGGCGGCGGCTTAACACATGCAAGTCGAGCGGTAGAGAAAGCTTGTCTC 60
QY 75 TTGAGAGCGGCGGCGGCTTAAGCTTAAGCTTAAGCTTAAGCTTAAGCTTAAGCTTA 134
DB 61 AATTGAGCGGCGGCGGCTTAAGCTTAAGCTTAAGCTTAAGCTTAAGCTTAAGCTTA 120
QY 135 TCGAAAGCGGCGGCTTAATACCGCATAGCTCTTACGGGAGAAAGCGGCGGCTT 194
DB 121 CTGAAAGCGGCGGCTTAATACCGCATAGCTCTTACGGGAGAAAGCGGCGGCTT 180
QY 195 TTGCGCTTACAGATGAGCGCTTGTGCGATTAAGCTTAAGCTTAAGCTTAAGCTTA 254
DB 181 TTGCGCTTACAGATGAGCGCTTGTGCGATTAAGCTTAAGCTTAAGCTTAAGCTTA 240
QY 255 GCGAGATCCGCTTAAGCTTGTGAGAGATGATCAGTACACCTGAACTGAGACACGCTCC 314
DB 241 GCGAGATCCGCTTAAGCTTGTGAGAGATGATCAGTACACCTGAACTGAGACACGCTCC 300
QY 315 AGACTCTTAAGCGGAGGCGGCTTAAGCTTAAGCTTAAGCTTAAGCTTAAGCTTAAG 374
DB 301 AGACTCTTAAGCGGAGGCGGCTTAAGCTTAAGCTTAAGCTTAAGCTTAAGCTTAAG 360
QY 375 CATGCCGCTTGTGAAGAAAGCTTGTGAGATTAAGCTTAAGCTTAAGCTTAAGCTTAAG 434
DB 361 CATGCCGCTTGTGAAGAAAGCTTGTGAGATTAAGCTTAAGCTTAAGCTTAAGCTTAAG 420
QY 435 TTGAGATTAATCTGCAATTTTGAAGTTTGAAGTTTGAAGTTTGAAGTTTGAAGTTT 494
DB 421 CATTAACTTAATCTGCAATTTTGAAGTTTGAAGTTTGAAGTTTGAAGTTTGAAGTTT 480
QY 495 TGCAGAGCGGCGGCTTAATACAGAGGCTGGAAGCTTAAGCTTAAGCTTAAGCTTAAG 554
DB 481 TGCAGAGCGGCGGCTTAATACAGAGGCTGGAAGCTTAAGCTTAAGCTTAAGCTTAAG 540
QY 555 GCGCGATGAGTGTGTTTGAAGTTTGAAGTTTGAAGTTTGAAGTTTGAAGTTTGAAGTT 614
DB 541 GCGCGATGAGTGTGTTTGAAGTTTGAAGTTTGAAGTTTGAAGTTTGAAGTTTGAAGTT 600
QY 615 TTCAAACTGACTAGATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTAT 674
DB 601 TTCAAACTGACTAGATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTAT 660
QY 675 ATGCGTATGATATGAGAGAAACACAGATGAGTATGAGTATGAGTATGAGTATGAGTAT 734
DB 661 ATGCGTATGATATGAGAGAAACACAGATGAGTATGAGTATGAGTATGAGTATGAGTAT 720
QY 735 CTGAGTGTGCGGAGGCGGCTTAAGCTTAAGCTTAAGCTTAAGCTTAAGCTTAAGCTTA 794
DB 721 CTGAGTGTGCGGAGGCGGCTTAAGCTTAAGCTTAAGCTTAAGCTTAAGCTTAAGCTTA 780
QY 795 ACGATGCTAAGCTTGTGAGAGCTTGTGAGAGCTTGTGAGAGCTTGTGAGAGCTTGTGAG 854
DB 781 ACGATGCTAAGCTTGTGAGAGCTTGTGAGAGCTTGTGAGAGCTTGTGAGAGCTTGTGAG 840

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QY 855 TGACCGCTGGGAGGCTAGCGGCGGCAAGCTTAATACTAAATGAAATTGACGGGGCGCCGA 914
DB 841 TGACCGCTGGGAGGCTAGCGGCGGCAAGCTTAATACTAAATGAAATTGACGGGGCGCCGA 900
QY 915 CAAGCGGTGAGAGATGTGTTTATTCGAAGCAACGGAAGAACTTACAGAGCTTGAC 974
DB 901 CAAGCGGTGAGAGATGTGTTTATTCGAAGCAACGGAAGAACTTACAGAGCTTGAC 960
QY 975 ATCCATGAACCTTCTAGAGATGATTTGCTTGGGAACTTGAAGACATTGAGACAGTGTGCA 1034
DB 961 ATCCATGAACCTTCTAGAGATGATTTGCTTGGGAACTTGAAGACATTGAGACAGTGTGCA 1020
QY 1035 TGCGTGTGCTAGCGCTGTGTTGTAATGTAAG 1068
DB 1021 TGCGTGTGCTAGCGCTGTGTTGTAATGTAAG 1054

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RESULT 4

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US-09-748-205-1
; Sequence 1, Application US/09748205
; Patent No. 6586562

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; GENERAL INFORMATION:
; APPLICANT: Canon Inc.
; TITLE OF INVENTION: Polyhydroxyalkanoate its manufacturing method, and microorganism
; FILE REFERENCE: 4351009
; CURRENT APPLICATION NUMBER: US/09/748,205
; CURRENT FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 1
; SEQ ID NO: 1
; LENGTH: 1501
; TYPE: DNA
; ORGANISM: Pseudomonas jessenii 161 strain.
; US-09-748-205-1

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```

Query Match      92.1% Score 985.2; DB 4; Length 1501;
Best Local Similarity 95.9%; Pred. No. 0;
Matches 1011; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

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QY 15 TGAACGCTGGCGGCGGCTTAACACATGCAAGTCGAGCGGTAGAGAAAGCTTGTCTC 74
DB 1 TGAACGCTGGCGGCGGCTTAACACATGCAAGTCGAGCGGTAGAGAAAGCTTGTCTC 60
QY 75 TTGAGAGCGGCGGCGGCTTAAGCTTAAGCTTAAGCTTAAGCTTAAGCTTAAGCTTA 134
DB 61 AATTGAGCGGCGGCGGCTTAAGCTTAAGCTTAAGCTTAAGCTTAAGCTTAAGCTTA 120
QY 135 TCGAAAGCGGCGGCTTAATACCGCATAGCTCTTACGGGAGAAAGCGGCGGCTT 194
DB 121 CTGAAAGCGGCGGCTTAATACCGCATAGCTCTTACGGGAGAAAGCGGCGGCTT 180
QY 195 TTGCGCTTACAGATGAGCGCTTGTGCGATTAAGCTTAAGCTTAAGCTTAAGCTTAAG 254
DB 181 TTGCGCTTACAGATGAGCGCTTGTGCGATTAAGCTTAAGCTTAAGCTTAAGCTTAAG 240
QY 255 GCGAGATCCGCTTAAGCTTGTGAGAGATGATCAGTACACCTGAACTGAGACACGCTCC 314
DB 241 GCGAGATCCGCTTAAGCTTGTGAGAGATGATCAGTACACCTGAACTGAGACACGCTCC 300
QY 315 AGACTCTTAAGCGGAGGCGGCTTAAGCTTAAGCTTAAGCTTAAGCTTAAGCTTAAG 374
DB 301 AGACTCTTAAGCGGAGGCGGCTTAAGCTTAAGCTTAAGCTTAAGCTTAAGCTTAAG 360
QY 375 CATGCCGCTTGTGAAGAAAGCTTGTGAGATTAAGCTTAAGCTTAAGCTTAAGCTTAAG 434
DB 361 CATGCCGCTTGTGAAGAAAGCTTGTGAGATTAAGCTTAAGCTTAAGCTTAAGCTTAAG 420
QY 435 TTGAGATTAATCTGCAATTTTGAAGTTTGAAGTTTGAAGTTTGAAGTTTGAAGTTT 494
DB 421 CATTAACTTAATCTGCAATTTTGAAGTTTGAAGTTTGAAGTTTGAAGTTTGAAGTTT 480
QY 495 TGCAGAGCGGCGGCTTAATACAGAGGCTGGAAGCTTAAGCTTAAGCTTAAGCTTAAG 554

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OY 435 TTGAGATTAACTCTGCACATTTTGACGTACCGACAGAAATTAAGACCGGGCTAACTCG 494
Db 421 CATTAACCTAATAGCTAGTGTGTTTGACGTTACCGAAGAAATTAAGACCGGGCTAACTCG 480
OY 495 TGCACAGACCCCGCGTAATACAGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAG 554
Db 481 TGCCAGACCGCGCGTAATACAGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAG 540
OY 555 CGCGGTAAGTGTGTTGTTAGTTGGATATGGAAATCCCGGGGCTCAACCTGGGAATCTGA 614
Db 541 CGCGGTAAGTGTGTTGTTAGTTGGATATGGAAATCCCGGGGCTCAACCTGGGAATCTGA 600
OY 615 TTCAAAACTGACTGACTAGTAGTATGTAGAGGGGTGTGTGAATTTCTGTGTAGCGGTGA 674
Db 601 TTCAAAACTGAACAAGCTAGTAGTATGTAGAGGGGTGTGTGAATTTCTGTGTAGCGGTGA 660
OY 675 ATGGGTGATATTAAGGAAGAAACACCACTGGCGAAAGCGACACCTGTGACTAATACTGA 734
Db 661 ATGGGTGATATTAAGGAAGAAACACCACTGGCGAAAGCGACACCTGTGACTAATACTGA 720
OY 735 CTGAGGTGCGAAACCGTGGGGGCAAAACAGGATTAGTACCTGTAGTCCAGCGGTAA 794
Db 721 CTGAGGTGCGAAACCGTGGGGGCAAAACAGGATTAGTACCTGTAGTCCAGCGGTAA 780
OY 795 ACGATGTCAATACGCGGTGGAGACCTTTAGCTTTTAGTGGCCAGCTAAACGATTAACT 854
Db 781 ACGATGTCAATACGCGGTGGAGACCTTTAGCTTTTAGTGGCCAGCTAAACGATTAACT 840
OY 855 TGACCGGCTGGGGAGTACCGGCGCAAGTTAAACTCAATTAATTAAGCGGGGGCCCGGA 914
Db 841 TGACCGGCTGGGGAGTACCGGCGCAAGTTAAACTCAATTAATTAAGCGGGGGCCCGGA 900
OY 915 CAAGCGGTGAGCATGTGTTTAATTGGAACCAACGGGAAGAACTTACCGAGCCTTGA 974
Db 901 CAAGCGGTGAGCATGTGTTTAATTGGAACCAACGGGAAGAACTTACCGAGCCTTGA 960
OY 975 ATCAATGAATTTCTAGAGATAGATGTGGCCTCGGGAACTTGAACAGTGTCTGA 1034
Db 961 ATCAATGAATTTCTAGAGATAGATGTGGCCTCGGGAACTTGAACAGTGTCTGA 1020
OY 1035 TGAGTGTCTGAGCTGCTGTGTGTAATGTAAAG 1068
Db 1021 TGAGTGTCTGAGCTGCTGTGTGTAATGTAAAG 1054

RESULT 2
US-09-821-016-5
; Sequence 5, Application US/09821016
; Patent No. 6485951
; GENERAL INFORMATION:
; APPLICANT: CANON INC.
; TITLE OF INVENTION: Polynhydcoxalkanoate Synthase and Gene Encoding the Same Enzyme
; FILE REFERENCE: 4051021
; CURRENT APPLICATION NUMBER: US/09/821,016
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Microsoft Word
; SEQ ID NO 5
; LENGTH: 1501
; TYPE: DNA
; ORGANISM: Pseudomonas jessenii Pl61 ; BP-7376
; FEATURE:
; US-09-821-016-5

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	Query March Best Local Similarity Matches 1011; Conservative	92.1%; 95.9%; 0;	Score 985.2; Pred. NC. 0; Mismatches	DB 4;	Length 1501; Indels 43;	Gaps 0;
Qy	15 TGAAGCCTGGCGGAGCCCTACACATCAAGTCGACGGTAGAGAGAACTTGGCTTTC					74
Db	1 TGAACCTTCGGCGGACCTTACACATCAAGTCGAGGGATGACGGACCTTGGCTTCCG					60
Qy	75 TTGAGACGGGCGGACGGGTAGATGCTGCTTGGATCTTGCCTGGTAGTGGGGGATTAAGCT					134

Db	61	AATTCAAGCGCGGAGCGGGTGAAGTAATGCTTGAAGAACTGCTGGTAACTGGGGGACAACGT	120
Qy	135	TCGGAAAACGACCGCTAATACCGCATACGCTCTACCGGAGAAAGCAGGGGACCTTCGGGGC	194
Db	121	CTCGAAAAGGAGCGCTAATATACCGCATACGCTCTACCGGAGAAAGCAGGGGACCTTCGGGGC	180
Qy	195	TTGGGCTATCAGATGAGCCTTAGTGGATTGAGCTAATGTTGGTGAAGTAAATGGCTCAACAA	254
Db	181	TTGGGCTATCAGATGAGCCTTAGTGGATTGAGCTAATGTTGGTGAAGTAAATGGCTCAACAA	240
Qy	255	GGCAGCATCCGTAACTGCTGAGAGATGATCAGTACACATGAGAACTGAGACAGGTCC	314
Db	241	GGCAGCATCCGTAACTGCTGAGAGATGATCAGTACACATGAGAACTGAGACAGGTCC	300
Qy	315	AGACTCTTACGGGAGGCGACAGTGGGGAAATTGGAACATGGCGGAAAGCTGATCCAGC	374
Db	301	AGACTCTTACGGGAGGCGACAGTGGGGAAATTGGAACATGGCGGAAAGCTGATCCAGC	360
Qy	375	CATGCGCGGTGTGTAAGAAAGGCTTCGCGAATTGTAAAGCATTTAAGTTGGGAGGAGGG	434
Db	361	CATGCGCGGTGTGTAAGAAAGGCTTCGCGAATTGTAAAGCATTTAAGTTGGGAGGAGGG	420
Qy	435	TTGTAGATTAACTCTGCAATTTTGACGTTACCGACAGATAAGACAACCGCTAACTCG	494
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Qy	495	TGCGACACACCGCGGTAAATACAGAGGGTGAAGGCTTAATCCGAATTACTGGGCGTTAAG	554
Db	481	TGCGACACACCGCGGTAAATACAGAGGGTGAAGGCTTAATCCGAATTACTGGGCGTTAAG	540
Qy	555	CGGCGGTAGGTGTTGTTAAATTGCAATGTAATCCCGGGCTCAACCTGGGAACTGCA	614
Db	541	CGGCGGTAGGTGTTGTTAAATTGCAATGTAATCCCGGGCTCAACCTGGGAACTGCA	600
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Db	661	ATGCTGATATATAGAGAGGAAACACAGAGGCGGAAGCGCACCTCGATTAATATGACA	720
Qy	735	CTGAGGTGGAATAGCGTGGGGAGCAAAACAGGATTAATACCTCGTATGTCACGCCGTAA	794
Db	721	CTGAGGTGGAATAGCGTGGGGAGCAAAACAGGATTAATACCTCGTATGTCACGCCGTAA	780
Qy	795	ACGATGTCAACTAGCCGTTGGAAGCGTTGAGCTTTTAGTGGCGCACCTAAGCATTAAT	854
Db	781	ACGATGTCAACTAGCCGTTGGAAGCGTTGAGCTTTTAGTGGCGCACCTAAGCATTAAT	840
Qy	855	TGACCGCCTGGGGAGTACGAGCCGACAGGTTAAATCTCAATGTAATTGACCGGGGCCGCA	914
Db	841	TGACCGCCTGGGGAGTACGAGCCGACAGGTTAAATCTCAATGTAATTGACCGGGGCCGCA	900
Qy	915	CAAGCGGTGACATAGTGGTTTAATTGGAAGCAACCGAGAACTTACCAAGGCTTGAC	974
Db	901	CAAGCGGTGACATAGTGGTTTAATTGGAAGCAACCGAGAACTTACCAAGGCTTGAC	960
Qy	975	ATTCATATGAATCTTTATAGATATGATTGTGCTTCGGAACATTAGACAGAGTGTGCA	1034
Db	961	ATTCATATGAATCTTTATAGATATGATTGTGCTTCGGAACATTAGACAGAGTGTGCA	1020
Qy	1035	TGGCTGTCTCAGCTCGTGTGTGTAATGTAAAG	1068
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RESULT 3
US-09-745-476-1
; Sequence 1, Application US/09745476
; Patent No. 6521429
; GENERAL INFORMATION:

Mon Feb 2 10:57:13 2004

us-09-737-297-2.rst

Page 12

QY	63	GGTAGAGGGGTTGGGAAATTTCTGTGTAGCGGTGAAATGCGTAGATATAGGAAGAAAC	638
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Db	353	CAACGGCGAAAGCACTGTGTGGGCGGACACTGACACTGAGAGAGAAAGCTAGGGAGC	294
QY	759	AACCAAGATTAGTACCCTGGTAGTCCACGCGGTAAACGATGTCAACTAGCCGTTGAAAG	818
Db	293	GATGGGATTAGTATACCCAGTAGTCTTAGCCGTAAAGATGATGATCTAGAGCGCTGTGCG	234
QY	819	CGTTGA-GCTTTTAGTGGCGCAGCTAATGACATTAAGTGAACGCGCTGGGGAGTACGCGCG	877
Db	233	TATCGACCCGTGACAGTCTGTAGCTTAGACCGTTAGTATCCCGCTGGGGAGTACGTTGG	174
QY	878	CAAGGTTAAACTCAATGATATTTGACGGGGGCCCGACACACCGGTGAGCATGTGTTTA	937
Db	173	CAAGATGAAACCTCAAGGAATTGACGGGGGCCCGACACACCGGTGAGCATGTGTTTA	114
QY	938	ATTTCGAAGCAACCGGAAGACTTACAGAGCCTTGACATTCATATGAATTTCATAGAGATA	997
Db	113	ATTTCGATGCAAACCGGAAGACTTACAGAGCCTTGACATTCACCGGAATTCCTTGAAGA	54
QY	998	GATTGATGCGCTCGGGACATTTGAGACAGGTGCTGCATGCTGTGCTCAAGTCTC	1050
Db	53	GAGGGGTGCTTTGGAAACGGGACACAGGTGTCATGCTGTGCTCAAGTCTC 1	

Search completed: January 30, 2004, 23:43:18
Job time : 2518.83 secs

D	96	GGGAAACACCAGTGGAAA	CGGCTCTAATACCCCGTAGGCTGAGGACAAAGAGGAA	902
Q	183	GACCTTCGGGCGCTTGCGTATCAATAGAGCCTAAGTGGATTGATAGTGGTGAAGTAA	242	
D	901	TCGCCCCGAG-----GAGGGGCTCGCGCTGTATGTATGCTATGTGGTAGGCA	855	
Q	243	TGGCTACCAAGCGCGACGATCCGTAACAGTGTCTAGAGAGATGATCACTCACTGGAACT	302	
D	854	TAGCTTACCAAGCGCGATGATCAGTATGCTGTGCTCGAGAGATGATCAAGCCACACTGGAACT	795	
Q	303	GAGACACGGTCCAGATCCTTACGGGAGGACAGCACTGGGGAAATATGGAACAATGGCGGAA	362	
D	794	GAGACACGGCGCGATCTCTACGGGAGGACAGTGGGAAATTTCCGAATGGCGGAA	735	
Q	363	GCGTGAATCCAGCATCCCGCTGTGTGAAGAGGCTCTTCGAAATGTGTAAGCACTTTAAGT	422	
D	734	GCTTACGAGAGCAATCCCGCTGTGAGAGTAAAGGCTTACGGTCTCGAACTTTCTTTCC	675	
Q	423	TGGAGAGAGGGTTGTATATTAATCTCGAATTTTGAGGTTAACCGACAATTAAGAC	482	
D	674	AGAGAGAGAG-----CAATGACGGATATCTGGGAGATTAAGAT	638	
Q	483	CGGCTAATCTGTGACGAGAGCGCGGTATATCAAGAGGTGCAAGCGTTATCGAATTA	542	
D	637	CGGCTAATCTGTGACGAGAGCGCGGTATATCAAGAGGTGCAAGCGTTATCGAATTA	578	
Q	543	CTGGCGTAAAGCGCGGTAGGTGTTGTTAAGTTGATGTGAATCCCGGGCTCAAC	602	
D	577	TTGGCGTAAAGCGGTGTATAGTGGCTTTTAAATCGCGCTCAATCCAGGGCTCAAC	518	
Q	603	CTGGGAATCGATCAAACTGATCAGTACATAGATGTGAGGGGTGTGGAATTTCCG	662	
D	517	CTTGGACAGCGGTGTGAATCTCAAGCTTGAATGCGTGGGGCAGAGGAAATTTCCG	458	
Q	663	TGTAGCGGTGAATGCGTATATAGAGAGAACACAGTGGCGAAGGCCACCACTTGA	722	
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Q	962	ACGAGGCTTGAATCAATGAATCTTTAGAGTAAATTTGATGTTGTCCTTGGGAACATTGA	1021	
D	157	ACGAGGCTTGAATCAATCCCGCAATCTCTTGAAGAGAGGGGTGCTTCGGGAACCGGA	98	
Q	1022	GACAGGTGTCGATGGCTGTGCTACAGCTCGTGTGTGAATTTGTAAG	1068	
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ACCESSION	BOWND507R_BO_2_3			GSS 20-FEB-2007
VERSION	BH700021			
KEYWORDS	BH700021.1	GI:18775982		
SOURCE	GSS.			
ORGANISM	Brassica oleracea			
	Brassica oleracea			
	Brassica oleracea			

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids 1 (bases 1 to 995)	Whole genome shotgun sequencing of <i>Brassica oleracea</i>	Unpublished	
2	Town, C.D., Van Aken, S., Utteback, T., Koo, H. and Fraser, C.M.		Other GSSEs: BOMND50TF	
3	TRGR		Contact: Chris Town	
4	9712 Medical Center Drive, Rockville, MD 20850, USA.			
5	Tel: 301-838-3523			
6	Fax: 301-838-0202			
7	Email: cdtown@trg.org			
8	DNA is from a doubled haploid provided by Tom Osborn.			
9	Seq primer: 7R			
10	Class: sheared ends.			
11	Location/Qualifiers			
12	1..995			
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21	ORIGIN			258 t
22	Query Match	49.7%	Score 531.6;	DB 28; Length 995;
23	Best Local Similarity	73.0%	Pred. No. 6.6e-144;	
24	Matches 739;	Conservative 0;	Mismatches 237;	Indels 37; Gaps 3;
25	Oy	39	CATGCAAGTCGACCGGTAGAGAGAAGCTTCCTCTCTGAGAGCGGCGGACGGTGAAGTA	98
26	Db	977	CATGCTTACATCAATCAAGTCCGACGGGAAGTGTGTTTCAGTGGCGGACGGGTGAATC	918
27	Oy	99	ATGCTTAGAATTCCTCTGTGTAGTGTGGGGATTAACGTTGGAAACGACCTTAATACCGCA	158
28	Db	917	ACCGCTAAMACCTCCCTCGAGAGGGGAAACAAACAGCTGMAACGGCTCTAATACCCCG	858
29	Oy	159	TACGTCCTACGGGAAAGACAGGGGACCTTCGGGCTTGCGCTACAGATGACCTAGGT	218
30	Db	857	TAGCTGAGAGACCAAAAGAGAGATCCGCCGAG-----GAGGGGCTCGGCT	811
31	Oy	219	CGGATTAGTACTGCTGTAGGTAATGCTCAACCAAGCGACGATCCGTACTGTGCTGAG	278
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33	Oy	279	AGGATGATCAGTCACTGGAACCTGACACACAGGTCGACACTCCTACGGAGGACACAGTG	338
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35	Oy	339	GGGAATATTGACATGGGCGAAAGCTGTATCCAGCGATCCGCGTGTGAAGAAGTCT	398
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Seq primer: TR
Class: sheared ends.

FEATURES

Location/Qualifiers
source

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/db_xref="taxon:3712"
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/note="Vector: pBOS1; Site:1: BstXI, 1.6-2 kb sheared
total DNA inserted into pBOS1 using BstXI linkers"

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Best Local Similarity 72.6%; Pred. No. 1.7e-146; Indels 48; Gaps 4;
Matches 775; Conservative 0; Mismatches 244;

QY 3 CCTTGCTCAGATTGAACGCTGGCGGAGGCTTACACATGCAGAGTGAAGGAGAGA 62
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QY 63 AGCTTGCTCTCTGAGAGCGGAGCGGCTGAGTAATGCTTAGAATCTCCCTGTAAGT 122
DB 993 -----GTGGTGTTCAGTGGCGGAGCGGCTGAGTAATGCTTAGAATCTCCCTGTAAGT 940
QY 123 GGGGATTAACGTTCCGAAACGACGCTATACCGCATACGCTCTACCGGAGAAACAGAGG 182
DB 939 GGGGATTAACGTTCCGAAACGACGCTATACCGCATACCGCTGAGGAGGAGGAGGAGGAGGAA 880
QY 183 GACCTTGGGCGCTGGGCTATCAGATGAGAGCTAGTCCGATTAGTGTAGTGAAGTAA 242
DB 879 TCCGCGCGAG-----GAGGCGCTCGCTGATTAGTGTAGTGAAGTAA 833
QY 243 TGGCTCAGCAGGCGAGCGATCCGTAAGTGTGAGAGATGATCAGTCACTGAGAACT 302
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QY 303 GAGACACGCTCCAGACTCTTACGAGGAGGAGAGTGGGAAATATTGACAAATGGGCGAAA 362
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QY 783 TCCACGCGCGTAAAGCATGTCAAATGCGGTTGAAGCCTTGA-CCTTTTAGTGGCGGAGC 841

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DB 255 TAACCGTTAAGTTGACCGCTGGGAGTACGCGCGGAGGTTAAATCTCAATGATTTG 196
QY 902 ACGGAGGCGCGGAGGAGGAGGAGTGTGTTAATGAGAGCAACGCGGAGACCTT 961
DB 195 ACGGAGGCGCGGAGGAGGAGGAGTGTGTTAATGAGAGCAACGCGGAGACCTT 136
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genomic survey sequence.
ACCESSION
BZ469058
VERSION
BZ469058.1 GI:26764665
KEYWORDS
GSS.
SOURCE
Brassica oleracea
ORGANISM
Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
eustroside II; Brassicales; Brassicaceae; Brassica.
REFERENCE
1 (bases 1 to 1106)
TOWN,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished
Other GSSs: BONH54TR
COMMENT
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TP
Class: sheared ends.

FEATURES
source

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total DNA inserted into pBOS1 using BstXI linkers"

BASE COUNT
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Query Match 50.4%; Score 539.8; DB 29; Length 1106;
Best Local Similarity 73.2%; Pred. No. 2.9e-146; Indels 49; Gaps 5;
Matches 781; Conservative 0; Mismatches 237;

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 Db 70 TCAGCTCGTGTGTGTAATGTGCG 46

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 VERSION GSS.
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 SOURCE Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 ORGANISM Pseudomonas aeruginosa
 REFERENCE 1 (bases 1 to 1072)
 AUTHORS Spencer,D.H., Raymond,C.K., Smith,E.E., Sims,E.F., Hastings,M.,
 Burns,J.U., Kaul,R. and Olsen,M.V.
 TITLE Whole-Genome-Sequence Variation among multiple isolates of
 Pseudomonas aeruginosa library
 JOURNAL J. Bacteriol., (2002) In press
 COMMENT Contact: Chris K. Raymond
 Genome Center
 University of Washington
 Box 352145, Seattle, WA 98105-2145, USA
 Tel: 2062216954
 Fax: 2066857244
 Email: craymond@u.washington.edu
 Class: shotgun.
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BASE COUNT 273 a 233 c 313 g 252 t 1 others
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 Best Local Similarity 88.6%; Pred. No. 1,1e-148;
 Matches 616; Conservative 0; Mismatches 76; Indels 3; Gaps 2;
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 QY 486 -CTGATCCAGCATGCGCGTGTGTAAGAGGCTTCCGATTTGTAAGCACTTTAAGT 544
 Db 423 TGGAGAGAGGCTTGAATTAATCTGCAATTTGACGTTCCGACAGATTAAGC 482
 QY 545 TGGAGAGAGGCTTGAATTAATCTGCAATTTGACGTTCCGACAGATTAAGC 604
 Db 483 CGGCTAATCTGTGCCAGGCGCGGTAAATACAGAGGCTGAAGCGTTAAATCGGAATTA 542
 QY 605 CGGCTAATCTGTGCCAGGCGCGGTAAATACAGAGGCTGAAGCGTTAAATCGGAATTA 664
 Db 543 CTGGCGGTAAAGGCGCGGTAAATCTGCTGTAAGTGAATATCCCGGGCTCAAC 602
 QY 665 CTGGCGGTAAAGGCGCGGTAAATCTGCTGTAAGTGAATATCCCGGGCTCAAC 724
 Db 603 CTGGCAATCTGCTAAATCTGCTGTAAGTGAATATCCCGGGCTCAAC 660
 QY 725 CTGGCAATCTGCTAAATCTGCTGTAAGTGAATATCCCGGGCTCAAC 784
 Db 661 TGTGTACCGGTGAATGCTTAATTTAGGAAGAA 695
 QY 785 TGTGTACCGGTGAATGCTTAATTTAGGAAGAA 819

RESULT 13
 B2474941/c 1069 bp DNA linear GSS 13-DEC-2002
 LOCUS BONKRS59TR_BO_1.6_2_XE_tot Brassica oleracea genomic clone BONKRS59,
 DEFINITION B2474941
 ACCESSION B2474941
 VERSION B2474941.1 GI:26776372
 KEYWORDS GSS.
 SOURCE Brassica oleracea
 ORGANISM Brassica oleracea
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 ; eurosids II; Brassicales; Brassicaceae; Brassica.
 REFERENCE 1 (bases 1 to 1069)
 AUTHORS Town,C.D., Van Aken,S., Utechtack,T., Koo,H. and Fraser,C.M.
 TITLE Whole genome shotgun sequencing of Brassica oleracea
 JOURNAL Unpublished
 COMMENT Other_GSSs: BONKRS59TF
 Contact: Chris Town
 TIGR

3712 Medical Center Drive, Rockville, MD 20850, USA.
 Tel: 301-838-3523
 Fax: 301-838-0208
 Email: cdtown@tigr.org
 DNA is from a doubled haploid provided by Tom Osborn.

BF845685 559 bp mRNA linear EST 16-JAN-2001
 LOCUS 780B5 cDNA from differential display on Platinum-treated embryos
 DEFINITION Xenopus laevis cDNA, mRNA sequence.
 ACCESSION BF845685
 VERSION BF845685.1 GI:12232824
 KEYWORDS EST.
 SOURCE Xenopus laevis (African clawed frog)
 ORGANISM Xenopus laevis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
 Xenopodinae; Xenopus.
 REFERENCE 1 (bases 1 to 559)
 Monetti, C., Vigetti, D., Gornati, R., Prati, M. and Bernardini, G.
 Platinum toxicity and gene expression in Xenopus embryos: analysis
 by FETAX and differential display
 JOURNAL Unpublished
 COMMENT Contact: Monetti C
 Department of Structural and Functional Biology
 University of Insubria
 Via Dunant 3, 21100, Varese, Italy
 Tel: ++3932421328
 Fax: ++3932421300
 Email: cmonetti@uninsubria.it.
 Location/Qualifiers
 1..559
 /organism="Xenopus laevis"
 /mol_type="mRNA"
 /db_xref="taxon:8335"
 /tissue_type="Whole 5-days embryos"
 /clone_lib="cDNA from differential display on
 Platinum-treated embryos"
 BASE COUNT 155 a 111 c 174 g 119 t

Query Match 52.1%; Score 557; DB 10; Length 559;
 Best Local Similarity 100.0%; Pred. No. 1.9e-151;
 Matches 557; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

253 AGGCGACGATCCGTAAGTGTGAGAGATGATGACATGACATGAGACCGGT 312
 3 AGGCGACGATCCGTAAGTGTGAGAGATGATGACATGACATGAGACCGGT 62
 313 CCAGACTCTTACGAGGAGGACAGAGAGTGGGAAATTGACATGAGGCGAAAGCCTGATCCA 372
 63 CCAGACTCTTACGAGGAGGACAGAGAGTGGGAAATTGACATGAGGCGAAAGCCTGATCCA 122
 373 GGCATGCGCGGTGTGAAAGAGTCTTCGATGTTAAAGCATTTAAGTTGGAGAGAA 432
 123 GGCATGCGCGGTGTGAAAGAGTCTTCGATGTTAAAGCATTTAAGTTGGAGAGAA 182
 433 GGTGTGATTAATCTCTGCAATTTTACGTTACCGACAGATTAACACCGGCTAATC 492
 183 GGTGTGATTAATCTCTGCAATTTTACGTTACCGACAGATTAACACCGGCTAATC 242
 493 TGTGCGACAGCGCGGTGTAACAGAGGTGCAACCGTTATCGGATTTCTGGCGGTAA 552
 243 TGTGCGACAGCGCGGTGTAACAGAGGTGCAACCGTTATCGGATTTCTGGCGGTAA 302
 553 AGCGCGGTAGGTGTTGTTAAGTTGATGTAATCCCGGAGCTCAACCTGGAACTG 612
 303 AGCGCGGTAGGTGTTGTTAAGTTGATGTAATCCCGGAGCTCAACCTGGAACTG 362
 613 CATTTAAATCTGACTAGATAGTATGTAAGGTGTGTAATTTCTGTGTAGCGGTG 672
 363 CATTTAAATCTGACTAGATAGTATGTAAGGTGTGTAATTTCTGTGTAGCGGTG 422
 673 AAATCGTAGATATAGAGAAACACAGTGGCGAAGCGACCACTGAGTAACTGA 732
 423 AAATCGTAGATATAGAGAAACACAGTGGCGAAGCGACCACTGAGTAACTGA 482
 733 CACTGAGTGGCAAAAGCGTGGGAGCAACAGATTGATCCCTGTGATCCACCGCGT 792

DB 483 CACTGAGTGGCAAAAGCGTGGGAGCAACAGATTGATACCTGTGATCCACCGCGT 542
 QY 793 AAAGATGTCACATGAC 809
 DB 543 AAAGATGTCACATGAC 559

RESULT 11
 LOCUS CD044496/c
 DEFINITION pSHB014XK10f.182390 pSHB: Infected hypocotyl soybean host. 48 hrs
 post infection Phytophthora sojae cDNA clone SHB014X10 5, mRNA
 sequence.
 ACCESSION CD044496
 VERSION CD044496.1 GI:30498089
 KEYWORDS EST.
 SOURCE Phytophthora sojae
 ORGANISM Phytophthora sojae
 Eukaryota; Stramenopiles; Oomycetes; Pythiales; Pythiaceae;
 Phytophthora.
 REFERENCE 1 (bases 1 to 674)
 Tyler, B.M., Judelson, H.S., Gijzen, M., Dean, R.A. and Maugh, M.E.
 USDA-IFARS: Expression of Phytophthora sojae genes during infection
 and propagation
 JOURNAL Unpublished
 COMMENT Contact: Tyler B
 Tyler Lab
 VBI
 1880 Pratt Dr., Blacksburg, VA 24061, USA
 Tel: 540-231-7318
 Email: bmttyler@vt.edu
 PCR primers
 FORWARD: BK reverse
 Plate: 014 row: K column: 10
 Seq primer: BK reverse
 High quality sequence stop: 674.
 Location/Qualifiers
 1..674
 /organism="Phytophthora sojae"
 /mol_type="mRNA"
 /db_xref="taxon:67593"
 /clone="SHB014X10"
 /tissue_type="infected host tissue"
 /cell_line="P6497"
 /dev_stage="48 hour post infection"
 /note="Vector: pBK-CMV; Site 1: EcoRI, Site 2: XhoI.
 USDA-IFARS: Expression of Phytophthora sojae genes during
 infection and propagation."
 BASE COUNT 148 a 206 c 149 g 170 t 1 others

Query Match 51.9%; Score 555.2; DB 14; Length 674;
 Best Local Similarity 93.0%; Pred. No. 7.1e-151;
 Matches 581; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

444 AATACCTGCAATTTTACGTTACCGACAGATTAACACCGGCTAATCTGTGCCAGCAG 503
 670 AATACCTGAGTTTACGTTACCGACAGATTAACACCGGCTAATCTGTGCCAGCAG 611
 504 CCGCGGTAAATACAGAGGTGCAACGTTATCGGATTTCTGGCGTAAAGCGCGGTG 563
 610 CCGCGGTAAATACAGAGGTGCAACGTTATCGGATTTCTGGCGTAAAGCGCGGTG 551
 564 GTGGTTGTTAAGTTGATGTAATCCCGGAGCTCAACCTGGAATGCAATTTCAAACT 623
 550 GTGGCTGATTAAGTTGATGTAATCCCGGAGCTCAACCTGGAATGCAATTTCAAACT 491
 624 GATCGAATAGATATAGAGAGGTGTGGAATTTCTGTGTAGCGGTAAATGCGTAA 683
 490 GTCTGCTAAGAGTGGGTAGAGGTGATGGAATTTCTCACTGTAGCGGTAAATGCGTAA 431

QY 111 CTG--CCTGGTAGTGGGGGATAACGTTGGAAAACGAGCGCTAATACCGCATACGCTTAC 168
DB 784 TTGGCCCTTGGTATGGGAAAACGTCGAGAACGGGCGCTAAACGGGAAACGCTCGA 725
QY 169 GGGAGAAA-GCAGGGGACCTTCGGGCTTCGCTATCAGATGAGCGTATGCTGATAGC 227
DB 724 GGGAGAAAAGGGGGGATCTTGGGACCCACCGCTTCAATGATGAGCTGATGATAGC 665
QY 228 TAAGTTGAGAGGTAATAGGCTCAACCAAGGGGAGC-ATCCGTAATCTGCTGAGAGATAT 286
DB 664 AAGTTGGTGGTAAAGGCCCTCCAGGAGGAACTCCCTACTTGGTCTTAAAGATGAT 605
QY 287 CAGTCACTGTAAGTGAAGCAGCGTCCAGACTCTCTCAAGGAGGAGCAGTGGGAAATAT 346
DB 604 CAGTCACTGTAAGTGAAGCAGCGTCCAGACTCTCTCAAGGAGGAGCAGTGGGAAATAT 545
QY 347 TGGACATGGGGGAGAAAGCTGATCCAGCCATGCGCGTGTGTGAAGAAAGTCTTGGAAT 406
DB 544 TGGACATGGGGGAGAAAGCTGATCCAGCCATGCGCGTGTGTGAAGAAAGTCTTGGAAT 485
QY 407 GTAAGCACTTAAAGTTGGAGGAGAGGTTGATTAATTAATCTGCAATTTTGAAGTTA 466
DB 484 GTAAAGCACTTAAAGTTGGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 425
QY 467 CCGACAGATTAAGCAGCGGCTAACTCTGTCAGCAGCGCGGTAATACAGAGGGTGCA 526
DB 424 CCAACAGATTAAGCAGCGGCTAACTCTGTCAGCAGCGCGGTAATACAGAGGGTGCA 365
QY 527 GCGTTATCGGAATTAATCTGGGCGTAAGGCGCGTAAGGCGTTTGTAAAGTTGATGTA 586
DB 364 GCGTTATCGGAATTAATCTGGGCGTAAGGCGCGTAAGGCGTTTGTAAAGTTGATGTA 305
QY 587 AATCCCGGCTCAACCTGGGAACTGATTAATACTGACTAGAGTAAGTGAAGG 646
DB 304 AATCCCGGCTCAACCTGGGAACTGATTAATACTGACTAGAGTAAGTGAAGG 245
QY 647 GTGTGGAATTTCTGTGTGAGCGGTAAATGCGTGAATATAGAAAGAAACACCAAGTGGC 706
DB 244 GTGTGGAATTTCTGTGTGAGCGGTAAATGCGTGAATATAGAAAGAAACACCAAGTGGC 185
QY 707 AAGGCGACCACTGAGCTAATTAATGACACTGAGGTGCAAGCGTGGGAGGAGGAGGAG 766
DB 184 AAGGCGACCACTGAGCTAATTAATGACACTGAGGTGCAAGCGTGGGAGGAGGAGGAG 125
QY 767 TTGATTAACCTGTGATGCAAGCGGTAAACGATGCACTAGCCGTTGGAAGCTTGAAGC 826
DB 124 CTGATTAACCTGTGATGCAAGCGGTAAACGATGCACTAGCCGTTGGAAGCTTGAAGC 65

RESULT 9
CD043647/c 699 bp mRNA linear EST 09-MAY-2003
LOCUS JSHB009XK05f.180500 JSHB: Infected hypocotyl soybean host. 48 hrs
DEFINITION post infection Phytophthora sojae cdna clone JSHB009X05 5, mRNA
sequence.
CD043647
VERSION CD043647.1 GI:30497240
KEYWORDS EST.
SOURCE Phytophthora sojae
ORGANISM Phytophthora sojae
Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
Phytophthora.
1 (bases 1 to 699)
REFERENCE Tyler B.M., Jungelson H.S., Gijzen M., Dean R.A. and Waugh M.E.
TITLE USDA-IPAFS: Expression of Phytophthora sojae genes during infection
and propagation
JOURNAL Unpublished
COMMENT Contact: Tyler B
Tyler lab
VBI
1880 Pratt Dr., Blackeburg, VA 24061, USA
Tel: 540-231-7318

Email: bmclyer@vt.edu
PCR Primers
FORWARD: BK reverse
Reverse: BK reverse
Plates: 009 row: K column: 05
Seq primer: BK reverse
High quality sequence stop: 699.
Location/Qualifiers
1..699
/organism="Phytophthora sojae"
/mol_type="mRNA"
/db_xref="taxon:67593"
/clone="JSHB009X05"
/tissue_type="infected host tissue"
/cell_line="P6497"
/dev_stage="48 hour post infection"
/clone_lib="JSHB: Infected hypocotyl soybean host. 48 hrs
post infection"
/note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI;
USDA-IPAFS: Expression of Phytophthora sojae genes during
infection and propagation."
BASE COUNT 153 a 212 c 156 g 178 t
ORIGIN
Query Match 52.2%; Score 559; DB 14; Length 699;
Best Local Similarity 92.2%; Pred. No. 5.6e-15;
Matches 589; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
QY 430 AAGGTTGATGATTAATCTGCAATTTTGAAGTACCGACAGATTAAGCAGCGGCTAA 489
DB 699 AAGGTTTACAGCAATACCTGTGATTTTACGTTACCGACAGATTAAGCAGCGGCTAA 640
QY 490 CTCTGTGCGAGAGCGCGGTAAATACAGAGGTTGCAAGCTTAAATCGGAATTAATCGGCG 549
DB 639 CTCTGTGCGAGAGCGCGGTAAATACAGAGGTTGCAAGCTTAAATCGGAATTAATCGGCG 580
QY 550 TAAAGCGCGTGAAGTGTGTTGTTAGTTGATGATGAAATCCCGGCTCAACCTGGGAA 609
DB 579 TAAAGCGCGTGAAGTGTGTTGTTAGTTGATGATGAAATCCCGGCTCAACCTGGGAA 520
QY 610 CTGCACTTCAAACTGACTGACTAGATGATGATGATGATGATGATGATGATGATGATG 669
DB 519 CTGCACTTCAAACTGACTGACTAGATGATGATGATGATGATGATGATGATGATGATG 460
QY 670 GTGAATGCGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 729
DB 459 GTGAATGCGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 400
QY 730 TGAACCTGAGTGGGAGAAAGCGTGGGAGCAACAGATTAATGATGATGATGATGATGATG 789
DB 399 TGAACCTGAGTGGGAGAAAGCGTGGGAGCAACAGATTAATGATGATGATGATGATGATG 340
QY 790 CGTAAACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 849
DB 339 CGTAAACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 280
QY 850 TAAAGTTGACCGGCTGGGAGTACCGGCCCAAGGTTAAATCAATGATGATGATGATGATG 909
DB 279 TAAAGTTGACCGGCTGGGAGTACCGGCCCAAGGTTAAATCAATGATGATGATGATGATG 220
QY 910 CCGCAGACCGGTTGAGAGTGTGTTTAAATGAAAGCAAGCGGAAAGCTTACAGAGCC 969
DB 219 CCGCAGACCGGTTGAGAGTGTGTTTAAATGAAAGCAAGCGGAAAGCTTACAGAGCC 160
QY 970 TTGACATCAATGAATCTTCTAGAGATGATGATGATGATGATGATGATGATGATGATGATG 1029
DB 159 TTGACATCAATGAATCTTCTAGAGATGATGATGATGATGATGATGATGATGATGATGATG 100
QY 1030 CTGATGAGTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1068
DB 99 CTGATGAGTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 61

RESULT 10

QY 894 ATGA 897
 DB 601 ATGA 604

RESULT 7
 LOCUS CD040169/c 641 bp mRNA linear EST 09-MAY-2003
 DEFINITION psfH032xK20f.293343 psfH: Infected hypocotyl soybean host. 48 hrs post infection Phytophthora sojae cDNA clone sHB032K20 5, mRNA sequence.

ACCESSION CD040169
 VERSION CD040169.1 GI:30502041
 KEYWORDS EST
 SOURCE Phytophthora sojae
 ORGANISM Phytophthora sojae
 Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae; Phytophthora.

REFERENCE 1 (bases 1 to 641)
 Tyler B.M., Judelson H.S., Gijzen M., Dean R.A. and Maugh M.B. USDA-IRAFs: Expression of Phytophthora sojae genes during infection and propagation
 Unpublished
 CONTACT: Tyler B
 JOURNAL
 COMMENT
 Tyler lab
 VBI
 1860 Pratt Dr., Blacksburg, VA 24061, USA
 Tel: 540-231-7318
 Email: bmtyle@vt.edu
 PCR Primers
 FORWARD: BK reverse
 Plate: 032 row: K column: 20
 Seq primer: BK reverse
 High quality sequence stop: 641.

FEATURES
 source
 location/Qualifiers
 1..641
 /organism="Phytophthora sojae"
 /mol_type="mRNA"
 /db_xref="taxon:67593"
 /clone="sHB032K20"
 /tissue_type="infected host tissue"
 /cell_line="P6497"
 /dev_stage="48 hour post infection"
 /clone_id="psfH: Infected hypocotyl soybean host. 48 hrs post infection"
 /note="Vector: pBK-CMV; Site 1: EcoRI; Site 2: XhoI; USDA-IRAFs: Expression of Phytophthora sojae genes during infection and propagation."
 BASE COUNT 135 a 199 c 142 g 164 t 1 others

ORIGIN
 Query Match 52.9%; Score 566.4; DB 14; Length 641;
 Best Local Similarity 96.3%; Pred. No. 3,7e-154;
 Matches 579; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 468 CGACGATTAAGCACCCTACTCTGTCCAGACGCGCGTAATACAGAGGTCACAG 527
 DB 641 CGACGATTAAGCACCCTACTCTGTCCAGACGCGCGTAATACAGAGGTCACAG 582
 QY 528 CGTATATCGAATTAAGTGGCGTAAAGCGCGCGTGGTGTGTTGAATGAGTGA 587
 DB 581 CGTATATCGAATTAAGTGGCGTAAAGCGCGCGTGGTGTGTTGAATGAGTGA 522
 QY 588 ATCCCCGGCTCAACCTGCGAAGCTGCATTCAAAACATCAATGATAGTATGTAAGG 647
 DB 521 ATCCCCGGCTCAACCTGCGAAGCTGCATTCAAAACATCAATGATAGTATGTAAGG 462
 QY 648 TGGTGAATTTCTGTGTAGCGGTGAATGCGTATATGAGAGAACACAGTGGCA 707
 DB 461 TGGTGAATTTCTGTGTAGCGGTGAATGCGTATATGAGAGAACACAGTGGCA 402
 QY 708 AGGGAGCACTGATATATCTACACTGAGGTGGCAAGCGTGGGAGCAACACGAT 767

DB 401 AGCGAACACCTGACCTGATTAATCTGACACTGAGGTGCGAAAGCTGGGAGCAACAGAT 342
 QY 768 TAGATACCTGTGTAGTCCAGCGCGTAACAGATGTCACTAGCCGTTGGAAGCTTGAGCT 827
 DB 341 TAGATACCTGTGTAGTCCAGCGCGTAACAGATGTCACTAGCCGTTGGAAGCTTGAGCT 282
 QY 828 TTTAGTGGCGGACCTAAGCATTAAGTTACCGGCTGGGGAGTACGGCGCAAGTTAA 887
 DB 281 CTTAGTGGCGGACCTAAGCATTAAGTTACCGGCTGGGGAGTACGGCGCAAGTTAA 222
 QY 888 ACTCAATGATTAAGCGGGGCGCCGACAAAGCGGTGAGCATGTGCTTTAAATTGCAACA 947
 DB 221 ACTCAATGATTAAGCGGGGCGCCGACAAAGCGGTGAGCATGTGCTTTAAATTGCAACA 162
 QY 948 ACCGGAAGACCTTACCAAGCGCTTGACATCCATGAATCTTTAAGATAGATTGGTCC 1007
 DB 161 ACCGGAAGACCTTACCAAGCGCTTGACATCCATGAATCTTTAAGATAGATTGGTCC 102
 QY 1008 TTGGGAACATTAAGACAGGTGTGATGCTGTGATGCTGTGATGCTGTGATGATGATG 1067
 DB 101 TTGGGAACATTAAGACAGGTGTGATGCTGTGATGCTGTGATGCTGTGATGATGATG 42
 QY 1068 G 1068
 DB 41 G 41

RESULT 8
 B2561605/c 1033 bp DNA linear GSS 17-DEC-2002
 LOCUS pacs2-164_3345_y2 pacs2-164 Pseudomonas aeruginosa genomic clone
 DEFINITION pacs2-164_3345, genomic survey sequence.
 ACCESSION B2561605
 VERSION B2561605.1 GI:27181948
 KEYWORDS GSS.
 SOURCE Pseudomonas aeruginosa
 ORGANISM Pseudomonas aeruginosa
 Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas.

REFERENCE 1 (bases 1 to 1033)
 Spencer D.H., Raymond C.K., Smith E.E., Sims E.E., Hastings M., Burns J.L., Kaul R. and Olsen M.V. Whole-Genome-Sequence variation among multiple isolates of Pseudomonas aeruginosa library J. Bacteriol. (2002) in press
 JOURNAL
 COMMENT
 Contact: Chris K. Raymond
 Genome Center
 University of Washington
 Box 352145, Seattle, WA 98105-2145, USA
 Tel: 2062216954
 Fax: 2066857244
 Email: craymond@u.washington.edu
 Class: Shotgun.

FEATURES
 source
 location/Qualifiers
 1..1033
 /organism="Pseudomonas aeruginosa"
 /mol_type="genomic DNA"
 /script="2-164"
 /db_xref="taxon:287"
 /clone="pacs2-164_3345"
 /clone_id="pacs2-164"
 /note="Tactical isolate 2-164 Whole genomic shotgun library."

BASE COUNT 216 a 313 c 223 g 280 t 1 others

ORIGIN
 Query Match 52.9%; Score 566.4; DB 29; Length 1033;
 Best Local Similarity 85.3%; Pred. No. 4.8e-154;
 Matches 665; Conservative 0; Mismatches 111; Indels 4; Gaps 3;

QY 51 GCGGTAGAGAGAGCTTCTCTCTCTGAGAGAGCGGCGGAGTATGCTAGAT 110
 DB 844 GAGATGAAGGAACTTCTCTCTCTGAGATCCACCGGAGCGGTGAGTATTCCTAGAA 785

Best Local Similarity 97.0%; Pred. No. 9.9e-156;
Matches 604; Conservative 0; Mismatches 17; Indels 2; Gaps 2;

QY 13 ATTGAACGCTGGCGGAGGCTTAACATGCAAGTCGAGCGGTAGAGAGAGCTTGTCTC 72
Db 20 ATTGAACGCTGGCGGAGGCTTAACATGCAAGTCGAGCGGTAGAGAGAGCTTGTCTC 79
QY 73 TCTTGAGAGCGGCGGAGCGGTGATGATGCTAGGATCTGCTTGTGATGAGGAGATAC 132
Db 80 TCTTGAGAGCGGCGGAGCGGTGATGATGCTAGGATCTGCTTGTGATGAGGAGATAC 139
QY 133 GTTCGGAACGAGCGGATATACCGCATACGCTTACCGGAGAGAGAGAGAGAGAGAGAG 132
Db 140 GTTCGGAACGAGCGGATATACCGCATACGCTTACCGGAGAGAGAGAGAGAGAGAGAG 139
QY 193 CTTTGGCTATCAGATGAGAGCTTACGATGATGATGATGATGATGATGATGATGATGAT 252
Db 200 CTTTGGCTATCAGATGAGAGCTTACGATGATGATGATGATGATGATGATGATGATGAT 259
QY 253 AGCGGACGATCCGCTAATCTGCTGAGAGAGATGATGATGATGATGATGATGATGATGAT 312
Db 260 AGCGGACGATCCGCTAATCTGCTGAGAGAGATGATGATGATGATGATGATGATGATGAT 319
QY 313 CCAGACTCTTACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 372
Db 320 CCAGACTCTTACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 379
QY 373 GCCATCCGCGGTGTGAGAGAGGCTTCTGATGATGATGATGATGATGATGATGATGATGAT 432
Db 380 GCCATCCGCGGTGTGAGAGAGGCTTCTGATGATGATGATGATGATGATGATGATGATGAT 439
QY 433 GGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 492
Db 440 GGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 499
QY 493 TGTGCGAGAGCGGCGGTATATACAGAGGCTGACGCTTAACTCGGATTTAGGCGCTAA 552
Db 500 TGTGCGAGAGCGGCGGTATATACAGAGGCTGACGCTTAACTCGGATTTAGGCGCGCTA 559
QY 553 AGGCGGCGGTAGGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 611
Db 560 AGGCGGCGGTAGGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 618
QY 612 GCATTCAGAACTGACTGACTAGA 634
Db 619 GCATTCAGAACTGACTGACTAGA 641

RESULT 6
BE204135 604 bp mRNA linear EST 05-SEP-2000
LOCUS EST196811 KV0 Medicago truncatula cDNA clone pKV0-1409, mRNA
DEFINITION sequence.
ACCESSION BE204135
VERSION BE204135
KEYWORDS EST: GI:8747418
SOURCE Medicago truncatula (barrel medic)
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eumecopsids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
Medicago.
1 (bases 1 to 604)
Vandenbosch, K., Endre, G., Huz, J., Moore, J., Beremand, P., Ellis, L.,
Town, C. D., Bowman, C. L., Craven, M. B., Hansen, T. S., Holt, I. E. and
Fraser, C. M.
ESTs from uninoculated seedling roots of Medicago truncatula
Unpublished
Contact: Vandenbosch K
Department of Plant Biology
University of Minnesota
220 Biosci Center, 1445 Gortner Ave, St. Paul, MN 55108, USA
Tel: 612 624 2755

Fax: 612 625 1738
Email: kvandenbosch@umn.edu
Texas A&M University name: T263907e
TIGR sequence name: MTG0537K
More information is available at:
http://chryse.tamu.edu/medicago
Seq primer: SKmod (CTA gaa cta gta gat cc).

FEATURES

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1..604
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/mol_type="mRNA"
/cultiivar="genotype A17"
/db_xref="taxon:3880"
/clone="pKV0-1409"
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/dev_stage="Immediately prior to inoculation with
Sinorhizobium meliloti (0 hour)"
/lab_host="E.coli strain XLOLR"
/clone_lib="XV0"

/note="Vector: Bluescript SK-; Site 1: EcoRI; Site 2:
XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
was directionally ligated into the Unizap XR vector from
stratagene and packaged using GigaPack III gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in XLOLR cells."

BASE COUNT

167 a 123 c 188 g 126 t

ORIGIN

Query Match 53.2%; Score 568.8; DB 10; Length 604;
Best Local Similarity 96.4%; Pred. No. 7.1e-155;
Matches 582; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 294 ACTGGAAGTGAACAGACCGCTCCAGCTCTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 353
Db 1 ACTGGAAGTGAACAGACCGCTCCAGCTCTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 60
QY 354 TGGGGAAGAGCGCTGATCCAGCATGCGCGGTGTGTGAAGAGGCTTCCGATTGTAAAGC 413
Db 61 TGGGGAAGAGCGCTGATCCAGCATGCGCGGTGTGTGAAGAGGCTTCCGATTGTAAAGC 120
QY 414 ACTTTAATTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 473
Db 121 ACTTTAATTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
QY 474 AATAAGCACCGGCTAACTCTGTGCGACAGCGCGGCTATATACAGAGGAGGAGGAGGAGGAGGAG 533
Db 181 AATAAGCACCGGCTAACTCTGTGCGACAGCGCGGCTATATACAGAGGAGGAGGAGGAGGAGGAG 240
QY 534 TGGGAATTAAGTGGGCGGTAAAGCGCGGTAGGTGTTGTTAAGTGTGAATATCCCG 593
Db 241 TGGGAATTAAGTGGGCGGTAAAGCGCGGTAGGTGTTGTTAAGTGTGAATATCCCG 300
QY 594 GGGCTCAACTGGGAGAGTGCATTCAGAACTGACTAGTAGTAGTAGTAGTAGTAGTAGTAGTAG 653
Db 301 GGGCTCAACTGGGAGAGTGCATTCAGAACTGACTAGTAGTAGTAGTAGTAGTAGTAGTAGTAG 360
QY 654 AATTTCCTGTGTAGCGGTGAATATCGTATATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 713
Db 361 AATTTCCTGTGTAGCGGTGAATATCGTATATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
QY 714 CCACCTGAGCTAATCTGACACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 773
Db 421 CCACCTGAGCTAATCTGACACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480
QY 774 CCTGTGATGTCACGCGGTAAACAGATGATCAATGACGCTTGAAGAGCTTGAAGCTTTAGT 833
Db 481 CCTGTGATGTCACGCGGTAAACAGATGATCAATGACGCTTGAAGAGCTTGAAGCTTTAGT 540
QY 834 GGGGAGCTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 893
Db 541 GGGGAGCTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600

DEFINITION 3B5 cDNA library of 4-day-old *Eucalyptus globulus* bicostata-Pisolithus tinctorius ectomycorrhiza Pisolithus tinctorius cDNA 5' similar to PMN-binding protein, mRNA sequence.

ACCESSION AM600903.1 GI:7304774

VERSION EST

SOURCE Pisolithus tinctorius

ORGANISM Pisolithus tinctorius
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes; Boletales; Sclerotidiales; Pisolithaceae; Pisolithus.

REFERENCE 1 (bases 1 to 660)
Voibret, C., Duplessie, S., Enceiot, N. and Martin, F.
Identification of symbiosis-regulated genes in *Eucalyptus globulus*-*Pisolithus tinctorius* ectomycorrhiza by differential hybridization of arrayed cDNAs

JOURNAL Plant J. 25 (2), 181-191 (2001)

MEDLINE 21097016

PUBMED 11169194

COMMENT Contact: Martin FM
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Institut National de la Recherche Agronomique
Centre INRA de Nancy, 54280 Champenoux, France
Tel: +33 383 39 40 80
Fax: +33 383 39 40 69
Email: fmartin@nancy.inra.fr
Insert Length: 660 Std Error: 0.00
Seq primer: Capfinder 5/CDS
POLY=No.

FEATURES

source

1..660
/organism="Pisolithus tinctorius"
/mol_type="mRNA"
/strain="441"
/db_xref="taxon:37468"
/issue_type="mantle and Hartig net hyphae"
/dev_stage="symbiotic, 4 days after contact"
/lab_host="Eucalyptus globulus bicostata"
/clone_id="cDNA library of 4-day-old *Eucalyptus globulus* bicostata-Pisolithus tinctorius ectomycorrhiza"
/note="Organ: ectomycorrhiza; Vector: pBluescript; Site: 1; EcoRI: The cDNA library was constructed from 1 ug total ectomycorrhiza RNA using the SMART cDNA library construction kit (#K1051.1, Clontech, Palo Alto, CA, USA) according to the manufacturer's instructions. cDNAs were cloned into EcoRI-digested pBluescript."

BASE COUNT 179 a 139 c 200 g 142 t

ORIGIN

Query Match 54.3%; Score 581; DB 9; Length 660;
Best Local Similarity 95.1%; Pred. No. 2e-158;
Matches 621; Conservative 0; Mismatches 30; Indels 2; Gaps 2;

QY 409 AAAGCACTTAAGTGGAGGAGGAGGTTGATTATTAATCTGCAATTTTGACGTTACC 468
DB 10 AAAGCACTTAAGTGGAGGAGGAGGATTAACCTTAACGTTGTCCTTGACGTTACC 69

QY 469 GACAGAAATAGCAACCGGCTAACTCTGTGCGACGACCGCGGTAATACAGAGGCGCAAGC 528
DB 70 GACAGAAATAGCAACCGGCTAACTCTGTGCGACGACCGCGGTAATACAGAGGCGCAAGC 129

QY 529 GTTAATCGAATTAAGTGGAGGAGGAGGCGGCTAGTGGTTGTTAATGATGATAA 588
DB 130 GTTAATCGAATTAAGTGGAGGAGGAGGCGGCTAGTGGTTGTTAATGATGATAA 169

QY 589 TCCCGGGCTCAACTGGGAACTGATTCATAAATGATGATGATGATGATGATGATGATGAT 648
DB 190 TCCCGGGCTCAACTGGGAACTGATTCATAAATGATGATGATGATGATGATGATGATGAT 249

QY 649 GTTGAATTTCTGTGTAGCGGTGAATGCGTAGATATAGAGAGGAAACACAGCGGCGAA 708
DB 250 AGTGAATTTCTGTGTAGCGGTGAATGCGTAGATATAGAGAGGAAACACAGCGGCGAA 309

QY 709 GGGGACCACTGAGACTAATATAGACTGAGGTGCGAAAGCGTGGGAGACAAACAGGATT 768

DB 310 GGGGACCACTGAGACTAATATAGACTGAGGTGCGAAAGCGTGGGAGACAAACAGGATT 369

QY 769 AGATACCTGTAGTACACCGCGTAACGATGTAACCTAGCCCTTGGAAGCCCTTGAGCTT 828

DB 370 AGATACCTGTAGTACACCGCGCGTAACGATGTAACCTAGCCCTTGGAAGCTTGAGACTC 429

QY 829 TTAGTGGCGCAGCTTAACGATTAAGTGAACCGCTGGGAGATGCGCCGCAAGTTTAA 888

DB 430 TTAGTGGCGCAGCTTAACGATTAAGTGAACCGCTGGGAGATGCGCCGCAAGTTTAA 489

QY 889 CTCAATTAATTAAGCGGCGCGCGCACAGCGGTGAGCATGTGTTAATGAGCA 948

DB 430 CTCAATTAATTAAGCGGCGCGCGCACAGCGGTGAGCATGTGTTAATGAGCA 548

QY 949 CGCGAAGAACTTACCAAGGCGCTTACATCCATGAATCTTCTAGATATGATGTCCT 1008

DB 549 CGCGAAGAACTTACCAAGGCGCTTACATCCATGAATCTTCTAGATATGATGTCCT 608

QY 1009 TCGGGAATTAAGCAAGGCTGCGATGCGTGTGATGCTGTTTGAAA 1061

DB 609 TCGGGAATTAAGCAAGGCTGCGATGCGTGTGATGCTGTTTGAAA 660

RESULT 5
BE636524 650 bp mRNA linear EST 25-AUG-2000
LOCUS SMOVL2CAS17H03SK Onchocerca volvulus L2 larvae cDNA (SAB98MLW-OVL2)
DEFINITION Onchocerca volvulus cDNA clone SMOVL2CAS17H03 5', mRNA sequence.

ACCESSION BE636524

VERSION BE636524.1 GI:9919635

KEYWORDS EST.

SOURCE Onchocerca volvulus

ORGANISM Onchocerca volvulus
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea; Onchocercidae; Onchocerca.

REFERENCE 1 (bases 1 to 650)
Williams, S.A.
Genes expressed in L2 larvae of *Onchocerca volvulus*

AUTHORS Unpublished

TITLE Contact: Steven A. Williams

JOURNAL Molecular Parasitology

COMMENT Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith College, Northampton, MA, 01063, USA
Tel: 413/5853826
Fax: 413/5853786
Email: genome@smith.edu

BASE COUNT 169 a 135 c 204 g 141 t 1 others

ORIGIN

Query Match 53.4%; Score 571.8; DB 10; Length 650;

FEATURES

source

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/organism="Onchocerca volvulus"
/mol_type="mRNA"
/db_xref="taxon:6282"
/clone="SMOVL2CAS17H03"
/dev_stage="L2"
/lab_host="X11-Blue MRF"
/clone_id="Onchocerca volvulus L2 larvae cDNA (SAB98MLW-OVL2)"
/note="Vector: Lambda Uni-ZAP XR; Site: 1; Eco RI; Site: 2; Xho I; Filarial nematode parasite of humans. mRNA was prepared from approximately 9,000 L2s isolated from infected mosquitoes from Kumba, Cameroon and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library has 7.3 x 10⁶ independent recombinants and the average insert size is approximately 1kb. The library was constructed by Michelle Lizotte-Waniewski. The library is available from Dr. S.A. Williams, email: genome@smith.edu."

QY 723 CTAAATGACACTGAGTGGCGAAAGCCGCGGAGCAACAGATTAGATACCTCGTAG 782
 Db 382 CTGACACTGACATGAGTGGCGAAAGCGTGGAGCAACAGATTAGATACCTCGTAG 323
 QY 783 TCGACCCCGGAAACGATGTCACACTAGCCGTTGGAAGCCTTGAGCTTTAGTGGCAGCT 842
 Db 322 TCGACCCCGGAAACGATGTCACACTAGCCGTTGGAAGCCTTGAGCTTTAGTGGCAGCT 263
 QY 843 AAGCAATTAGTTGACCCGCTGGGAGTACCGCCGAGAGTTAAACTCAATGAATGA 902
 Db 262 AAGCAATTAGTTGACCCGCTGGGAGTACCGCCGAGAGTTAAACTCAATGAATGA 203
 QY 903 CGGAGGCGCGCAACAGCGGTGGAGCATGTGTTAATTGAGCAACGGAAGACCTTA 962
 Db 202 CGGAGGCGCGCAACAGCGGTGGAGCATGTGTTAATTGAGCAACGGAAGACCTTA 143
 QY 963 CGAGGCTTGACATCCAAATGAATTTCTAGAGATAGATTGTGCTTGGGAAACATTGAG 1022
 Db 142 CTGGCCTTGACATGCTGAGAACTTTCAGAGATGATGTGCTTGGGAACTCAGAC 83
 QY 1023 ACGGTGCTGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1068
 Db 82 ACGGTGCTGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 37

RESULT 3
 LOCUS BH771024 6499 bp DNA linear GSS 01-MAY-2002
 DEFINITION LMGtag746 MG1363 Random Sequence Tag Library Lactococcus lactis
 subsp. cremoris genomic, genomic survey sequence.
 ACCESSION BH771024
 VERSION BH771024.1 GI:20373981
 KEYWORDS GSS.
 SOURCE Lactococcus lactis subsp. cremoris
 ORGANISM Lactococcus lactis subsp. cremoris
 Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 Lactococcus.

REFERENCE 1 (bases 1 to 6499)
 AUTHORS Bolotin A., Ehrlich, S.D. and Sorokin A.
 TITLE Studies of genomes of dairy bacteria Lactococcus lactis
 JOURNAL Sci. Aliments, (2002) In press
 COMMENT Contact: Sorokin A
 Genetique Microbiome

INRA
 CNU INRA, Domaine de Vilvert, 78352 Jouy en Josas cedex, France
 Tel: 33 1 34 65 25 16
 Fax: 33 1 34 65 25 21
 Email: sorokin@jouy.inra.fr
 best homologue in strain IL1403 is ymga (78%)
 Class: Shotgun
 High quality sequence start: 30
 High quality sequence stop: 6471.
 Location/Qualifiers

FEATURES

source
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 /organism="Lactococcus lactis subsp. cremoris"
 /mol_type="genomic DNA"
 /strain="MG1363"
 /db_xref="taxon:1359"
 /clone_id="MG1363 Random Sequence Tag Library"
 /note="Vector: pSGM2; Site 1: Small library of
 chromosomal fragments of L.lactis strain MG1363 was
 prepared by partial AluI digestion or by sonication."
 BASE COUNT 1946 a 1228 c 1683 g 1642 t

Query Match 55.3%; Score 591.4; DB 28; Length 6499;
 Best Local Similarity 75.0%; Pred. No. 6,4e-161;
 Matches 809; Conservative 0; Mismatches 256; Indels 14; Gaps 5;

QY 3 CCTTGCTCAGATTAAACGCTGCGGAGGCTTAACACATGCAAGTCGAGCGGTAGAGAGA 62
 Db 542 CCTGCTCAGACCAACGCTGCGGAGGCTTAATACATGCAAGTCGAGCGGTAGAGATT 601

QY 63 AGCTTG----CTTCTTGAGAGCGGGGAGACGGGTGATAGCTTA--GGATCTGCTTG 117
 Db 602 GGTGCTTGACCAATTATTAAAGACGGAACGGGTGATAGCTTA--GGATCTGCTTG 661
 QY 118 GTAAGTGGGGATTAAGTTGGAACGGAACGCTTAATACCGATAGCTCT-----ACGG 170
 Db 662 TAGACGGGGGACAAATTTGGAACGGAATGCTTAATACCGCAATTAATTAACATTAAG 721
 QY 171 GAGAAAGCAGGGGACCTTCGGGCCCTTGCGCATAGATGAGCCATAGGTGGATAGCTAG 230
 Db 722 TTTTAAATTGAAATGCAATTTGCATCTCAAAAGATGATCCGCGCTGATAGCTAG 781
 QY 231 TTGTAAGTAATGCTCAACAGGCGACATCCGTAATCTGCTGAGAGATGATCAGT 290
 Db 782 TTGCTAGGTAATAGCTCAACAGGCGATGATATATAGCCAGCTGAGAGAGGTGATCGGC 841
 QY 291 CACACTGGAATGAGACACGGTCCAGACTCTTAAGGAGGACAGCATGTGGGATATTGGA 350
 Db 842 CACATTGGGACATGAGACACGGCCCAACTCTTAAGGAGGACAGCATGTGGGATATTGGA 901
 QY 351 CAATGGGAGAAAGCTGATCCAGCCATCCGCGTGTGGAAGAGTCTTCGATTTGTA 410
 Db 902 CAATGAGCAAAAGCTGATCCAGCCATCCGCGTGTGGAAGAGTCTTCGATTTGTA 961
 QY 411 AGCACTTTAAGTTGGAGAGAGGTTGT-AGATTAAATCTCTCAATTTTGAAGCTTAACG 469
 Db 962 AACTCTGTTGTAGAGAAAGACGTTGTGAGAGTGAAGCTCAATCAAGTACGCTTAAC 1021
 QY 470 ACGAATTAAGACCGGCTTAACCTGTGACACAGCGCGGTAAATACAGAGGTGCAAGCG 529
 Db 1022 ACCCAAAAGGACCGCTTAACCTGTGACACAGCGCGGTAAATACAGAGGTGCAAGCG 1081
 QY 530 TTAATGGAATTAACCTGAGGTAAAGCGCGCTAGGTGTTTGTAACTGATGTAAT 589
 Db 1082 TTGTCCGGAATTAAT-GGGGGTAAAGCGAGCGAGGTGTTTAAATGCTGATTAAG 1141
 QY 590 CCGCGGCTCAACCTGAGGAATGCAATTCAAAATGACTGATTAAGTATGTTAAGGTG 649
 Db 1142 GCAATGCTCAACCTGGAATGGAATGCAATTCAAAATGACTGATTAAGTATGTTAAG 1200
 QY 650 GTGGAATTTCTGTGAGCGGTGAATGCTGATATAGAGAGAACACAGTGGCGAAG 709
 Db 1201 GTGGAATTTCTGTGAGCGGTGAATGCTGATATAGAGAGAACACAGTGGCGAAG 1260
 QY 710 GCGACCACTGGAATTAATCTGACACTGAGTGGCAAAAGCTGGGAGCAAAACGATTA 769
 Db 1261 GCGGCTCTCTGCTGTAATCTGACACTGAGTGGCAAAAGCTGGGAGCAAAACGATTA 1320
 QY 770 GATACCTGATGTCACAGCGCTTAACGATGCAACTGACGCTTGAAGCCTTAGAGCTT 829
 Db 1321 GATACCTGATGTCACAGCGCTTAACGATGCTGATGAGTGAAGAGCTAATAAGTCT 1380
 QY 830 TAGTGGCGAGCTTAACGATTAAGTTGACCGCTTGGGAGTACCGCCGCAAGGTTAAAC 889
 Db 1381 CTGATTCGAGCTTAACGATTAAGTTGACCGCTTGGGAGTACCGCCGCAAGGTTAAAC 1440
 QY 890 TCAATGAATTAAGCGGGGGCGCGCAACAGCGGTGAGAGATGTTAATTGCAAGCAC 949
 Db 1441 TCAATGAATTAAGCGGGGGCGCGCAACAGCGGTGAGAGATGTTAATTGCAAGCAC 1500
 QY 950 GCGAAGACCTTAACGAGGCTTGAATCAATGAATTTCTAGAGATGATGTGCTT 1009
 Db 1501 GCGAAGACCTTAACGAGGCTTGAATCAATGAATTTCTAGAGATGATGTGCTT 1560
 QY 1010 CGGGAACATTGAGACAGGCTGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1068
 Db 1561 CGGGAACATTGAGACAGGCTGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1619

RESULT 4
 LOCUS AM600903 660 bp mRNA linear EST 23-MAR-2000

source

1. .905
/organism="Pseudomonas aeruginosa"
/mol_type="genomic DNA"
/strain="MSH"
/db_xref="taxon:287"
/clone="msh2.2610"
/clone_lib="msh"
/note="Environmental isolate. Whole genomic shotgun library."
BASE COUNT 241 a 203 c 284 g 175 t 2 others

ORIGIN

Query Match 59.0%; Score 631; DB 29; Length 905;
Best Local Similarity 89.9%; Pred. No. 6.1e-173;
Matches 731; Conservative 0; Mismatches 77; Indels 5; Gaps 5;

QY 3 CCTTGCTCAGATTGAAACCGCTGCGGAGGCTTAACATGCAAGTCGAGCGGTAGAGAG 62
DB CATGGCTCAGATTGAAACCGCTGCGGAGGCTTAACATGCAAGTCGAGCGGTAGAGAG 153
QY 63 AGCTTGCTTCTCTTGAAGCGGCGGAGGCTGAGTAAATGCTAGAAATCTGCTGGTAGT 122
DB AGCTTGCTTCTCTTGAAGCGGCGGAGGCTGAGTAAATGCTAGAAATCTGCTGGTAGT 213
QY 123 GGGGGATAACGTTGGAAACGGAACGCTAATACCGCATACGCTTACCGGAGAAAGCAGAG 182
DB GGGGGATAACGTTGGAAACGGAACGCTAATACCGCATACGCTTACCGGAGAAAGCAGAG 273
QY 183 GACCTTGCGGCTTGGGCTATCAATAGAGCTAGTGGATTAGTGGTGGAGCTAA 242
DB GATCTTGAGACTCAAGCTATCAATAGAGCTAGTGGATTAGTGGTGGAGCTAA 333
QY 243 TGCTTACCAAGGCGACGATCCGTAATGCTGCTGAGAGATGATCACTCACTGAGACT 302
DB AGGCTTACCAAGGCGACGATCCGTAATGCTGCTGAGAGATGATCACTCACTGAGACT 393
QY 303 GAGAACGCTCCAGACTCTTACGAGGCGAGCACTGGGAAATATTGACAAATGGCGAAA 362
DB GAGAACGCTCCAGACTCTTACGAGGCGAGCACTGGGAAATATTGACAAATGGCGAAA 453
QY 363 GCGTATCCAGCATGCGCGGTGTGTGAAGAGCTTTCGATTGTAAACAATTAAAGT 422
DB GCGTATCCAGCATGCGCGGTGTGTGAAGAGCTTTCGATTGTAAACAATTAAAGT 513
QY 423 TGGAGAAAGGTTGTAGATTAAATCTCTGCAATTTTACGTTACCGACGAATTAAGAC 482
DB TGGAGAAAGGTTGTAGATTAAATCTCTGCAATTTTACGTTACCGACGAATTAAGAC 573
QY 483 CGGCTAATCTGTGCGACGAGCGGCGGTAAATACAGAGGTTGCAAGGCTTAATCGAATTA 542
DB CGGCTAATCTGTGCGACGAGCGGCGGTAAATACAGAGGTTGCAAGGCTTAATCGAATTA 633
QY 543 CTGGGCGTAAAGCGGCGGTAGTGGTTT-GTTAAAGTTGATGTGAAATCCCGGCTCAA 601
DB CTGGGCGTAAAGCGGCGGTAGTGGTTT-GTTAAAGTTGATGTGAAATCCCGGCTCAA 693
QY 602 CCGTGGAACTGCTCAAACTGAAGTGAATGATGATGATGATGATGATGATGATGATGATGAT 660
DB CCGTGGAACTGCTCAAACTGAAGTGAATGATGATGATGATGATGATGATGATGATGATGAT 753
QY 661 TGTGTAGCGGTGAAATGCGTAGATATAGAA-GGAAACCAATGCGGAGCCACACCT 719
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QY 720 GGAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 778
DB GGAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 873
QY 779 GTAGTCCAGCGCGTAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 811
DB GTAGTCCAGCGCGTAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 905
QY 874 GTAGTCCAGCGCGTAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 905

RESULT 2

CD042372/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

VBI

Tel: 540-231-7318

Email: dmtyle@vt.edu

PCR Primers

FORWARD: BK reverse

Plate: 040 row: F column: 24

Seg primer: BK reverse

High quality sequence stop: 741.

Location/Qualifiers

1. 741

/organism="Phytophthora sojae"

/mol_type="mRNA"

/db_xref="taxon:67593"

/clone="SHB040F24"

/tissue="infected host tissue"

/cell_line="P6487"

/dev_stage="48 hour post infection"

/clone_lib="PSHB: Infected hypocotyl soybean host. 48 hrs post infection"

/note="Vector: PBK-CMV; Site 1: EcoRI; Site 2: XhoI; USDA-IFARS: Expression of Phytophthora sojae genes during infection and propagation."

BASE COUNT 159 a 230 c 164 g 187 t 1 others

ORIGIN

Query Match 56.7%; Score 606.6; DB 14; Length 741;

Best Local Similarity 92.1%; Pred. No. 7.3e-166;

Matches 650; Conservative 0; Mismatches 55; Indels 1; Gaps 1;

QY 363 GCGTATCCAGCATGCGCGGTGTGTGAAGAGCTTTCGATTGTAAACAATTAAAGT 422
DB GCGTATCCAGCATGCGCGGTGTGTGAAGAGCTTTCGATTGTAAACAATTAAAGT 683
QY 423 TGGAGAAAGGTTGTAGATTAAATCTCTGCAATTTTGAAGTGAAGCAATTAAGAC 482
DB TGGAGAAAGGTTGTAGATTAAATCTCTGCAATTTTGAAGTGAAGCAATTAAGAC 623
QY 682 TGGAGAAAGGTTGTAGATTAAATCTCTGCAATTTTGAAGTGAAGCAATTAAGAC 623
DB TGGAGAAAGGTTGTAGATTAAATCTCTGCAATTTTGAAGTGAAGCAATTAAGAC 753
QY 483 CGGCTAATCTGTGCGACGAGCGGCGGTAAATACAGAGGTTGCAAGGCTTAATCGAATTA 542
DB CGGCTAATCTGTGCGACGAGCGGCGGTAAATACAGAGGTTGCAAGGCTTAATCGAATTA 563
QY 622 CCGGCTAATCTGTGCGACGAGCGGCGGTAAATACAGAGGTTGCAAGGCTTAATCGAATTA 563
DB CCGGCTAATCTGTGCGACGAGCGGCGGTAAATACAGAGGTTGCAAGGCTTAATCGAATTA 602
QY 543 CTGGGCGTAAAGCGGCGGTAGTGGTTT-GTTAAAGTTGATGTGAAATCCCGGCTCAA 602
DB CTGGGCGTAAAGCGGCGGTAGTGGTTT-GTTAAAGTTGATGTGAAATCCCGGCTCAA 503
QY 562 CTGGGCGTAAAGCGGCGGTAGTGGTTT-GTTAAAGTTGATGTGAAATCCCGGCTCAA 503
DB CTGGGCGTAAAGCGGCGGTAGTGGTTT-GTTAAAGTTGATGTGAAATCCCGGCTCAA 662
QY 603 CTGGGAACTGATCAAACTGAAGTGAATGATGATGATGATGATGATGATGATGATGATGAT 662
DB CTGGGAACTGATCAAACTGAAGTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 443
QY 502 CTGGGAACTGATCAAACTGAAGTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 443
DB CTGGGAACTGATCAAACTGAAGTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 722
QY 663 TGTAGCGGTAATGCGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 722
DB TGTAGCGGTAATGCGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 383
QY 442 TGTAGCGGTAATGCGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 383

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 30, 2004, 18:26:40 ; Search time 2513.83 Seconds
(without alignments)
10345.086 Million cell updates/sec

Title: US-09-737-297-2

Perfect score: 1070

Sequence: 1 gcccttgcacagatgcagc.....gtgttggaatgtaagggc 1070

Scoring table: IDENTITY_NUC

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
EST:
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_huc:*
9: gb_est1:*
10: gb_est2:*
11: gb_huc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pin:*
20: em_gss_vit:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_pig:*
27: em_gss_vtl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	631	59.0	905	29	B2572385 msh2_2610
2	606.6	56.7	741	14	CD042272 pshB040xf
3	591.4	55.3	6499	28	BH771024 LMGtag74
4	581	54.3	660	9	AW600903 3B5 CDNA

5	571.8	53.4	650	10	BE636524
6	568.4	52.9	604	10	BE204135
7	566.4	52.9	641	14	CD040169
8	566.4	52.9	1033	29	B2561605
9	559	52.2	699	14	CD043647
10	557	52.1	559	10	BF845685
11	555.2	51.9	674	14	CD044496
12	548	51.2	1062	29	B2558387
13	540.6	50.5	1077	29	B2474941
14	539.8	50.4	1106	29	B2469088
15	531.6	49.7	995	28	BH700021
16	526	49.2	1106	29	B2569556
17	523.8	49.0	716	29	CNS010Q8
18	518.6	48.5	1078	29	B2569555
19	517	48.3	1082	29	B2459110
20	515.6	48.2	947	29	B2464837
21	515.6	48.2	1020	28	BH688417
22	512	47.9	1079	28	BH705272
23	510.4	47.7	746	28	AQ957362
24	510	47.7	823	28	BH573967
25	508.2	47.5	862	28	BH527452
26	507.4	47.4	1010	29	B2431523
27	506.2	47.3	739	29	CNS01J02
28	502	46.9	716	28	AQ957363
29	501.8	46.9	833	28	BH540327
30	501.4	46.9	1323	29	B2575698
31	501.2	46.8	889	29	B2462275
32	501	46.8	1016	29	B2462201
33	501	46.8	1053	29	B2447500
34	499.2	46.7	848	28	BH730827
35	498.2	46.6	810	29	B2490808
36	497.2	46.5	553	14	CD047311
37	497	46.4	834	29	B2449239
38	497	46.4	861	29	B2464776
39	495.4	46.3	812	28	BH594258
40	493.8	46.1	823	29	B2498828
41	492.8	46.1	569	9	A1779239
42	492	46.0	857	28	BH579853
43	491.8	46.0	845	28	BH564435
44	487	45.5	814	28	BH555249
45	484	45.2	850	28	BH677382

ALIGNMENTS

RESULT 1
B2572385
LOCUS
DEFINITION msh2_2610.y2 msh Pseudomonas aeruginosa genomic clone msh2_2610,
genomic survey sequence.
ACCESSION B2572385
VERSION B2572385.1 GI:27207446
KEYWORDS
SOURCE
ORGANISM
Pseudomonas aeruginosa
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
REFERENCE
1 (bases 1 to 905)
Spencer,D.H., Raymond,C.K., Smith,E.E., Sims,E.E., Hastings,M.,
Burns,J.L., Kaul,R. and Olsen,M.V.
TITLE
Whole-Genome-Sequence Variation among multiple isolates of
Pseudomonas aeruginosa library
JOURNAL
J. Bacteriol. (2002) In press
COMMENT
Contact: Chris K. Raymond
Genome Center
University of Washington
Box 352145, Seattle, WA 98105-2145, USA
Tel: 2062216954
Fax: 2066857244
Email: craymond@u.washington.edu
Class: Shotgun.
Location/Qualifiers

FEATURES

XX 29-NOV-2000; 2000MO-US42391.
 XX 29-NOV-1999; 99US-0168150.
 XX (AVIB-) AVI BIOPHARMA INC.
 XX Iversen Pl;
 PI WPI; 2001-457295/49.
 DR
 XX
 XX Antibacterial compound, useful for treating bacterial infections and as
 PT livestock and poultry food supplement, comprises antisense
 PT oligonucleotides complementary to bacterial 16S and 23S rRNA -
 XX
 XX Disclosure; Page - ; 62pp; English.
 PS
 XX AAS1021-AAS1034 represent the coding sequences of bacterial 16S
 CC ribosomal RNA (rRNA) genes. The sequences were used to design anti-
 CC bacterial compounds comprising substantially unchanged antisense
 CC oligomers containing 8-40 nucleotide subunits, including a targeting
 CC nucleic acid sequence at least 10 nucleotides in length which is
 CC complementary to a bacterial 16S or 23S rRNA nucleic acid sequence.
 CC The antisense oligomers are used for treating a bacterial infection.
 CC In a human or a mammalian animal produced by *Escherichia coli*, *Salmonella*
 CC typhimurium, *Pseudomonas aeruginosa*, *Vibrio cholerae*, *Neisseria*
 CC gonorrhoeae, *Helicobacter pylori*, *Bartonella henselae*, *Haemophilus*
 CC tuberculosis, *Streptococcus pneumoniae*, *Treponema pallidum* and *Chlamydia*
 CC trachomatis. The antibacterial compound may be used as a food grain
 CC supplement in livestock and poultry food composition.
 CC Note: The present sequence is not shown in the specification but has
 CC been accessed from GenBank using the appropriate accession number given
 CC in the specification.
 CC
 XX
 SO Sequence 1467 BF; 370 A; 330 C; 458 G; 309 T; 0 other;

Query Match 84.8%; Score 907.4; DB 22; Length 1467;
 Best Local Similarity 93.9%; Pred. No. 1.2e-280;
 Matches 944; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 64 GCTTGCTTCTCTAGAGCGCGGAGTAAATGCTAGGAATGCTGCTGATAG 123
 DB 10 GCTTGCTTCTGATTCAGCGCGGAGTAAATGCTAGGAATGCTGCTGATAG 69
 QY 124 GGGGATACGTTGCGAAGCGAGCGTAAACCGCATACGTCCTACGCGAAGAAAGCAAGG 183
 DB 70 GGGGACACGTTTGAAAGGACGCTAAACCGCATACGTCCTACGCGAAGAAAGCAAGG 129
 QY 184 ACCTTGGGCTTGGCGTATCAGATGAGCTAGTGGATAGCTAGTGGATAGT 243
 DB 130 ACCTTGGGCTTGGCGTATCAGATGAGCTAGTGGATAGCTAGTGGATAGT 189
 QY 244 GGCTACCAAGGCGAGCATCGTAACTGTCTGAGAGATGATCACTGGAAC 303
 DB 190 GGCTACCAAGGCGAGCATCGTAACTGTCTGAGAGATGATCACTGGAAC 249
 QY 304 AGAAGCGTCCAGCTCTTACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 363
 DB 250 AGAAGCGTCCAGCTCTTACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 309
 QY 364 CCGATCAGGATGCGCGCTGTGTGAGAGAGGCTTGGATTTAAAGCACTTAAGTT 423
 DB 310 CCGATCAGGATGCGCGCTGTGTGAGAGAGGCTTGGATTTAAAGCACTTAAGTT 369
 QY 424 GGGAGGAAAGGCTTGAATTAATCTGCAATTTGACGTTACGAGAAATTAAGCAC 483
 DB 370 GGGAGGAAAGGCTTGAATTAATCTGCAATTTGACGTTACGAGAAATTAAGCAC 429
 QY 484 GGGTAACTGTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 543
 DB 430 GGGTAACTGTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 489

QY 544 TGGGCGTAAAGCGCGCTAGGCTGTTTGTAGTTGATGTAATCCCGGGCTGACC 603
 DB 490 TGGGCGTAAAGCGCGCTAGGCTGTTTGTAGTTGATGTAATCCCGGGCTGACC 549
 QY 604 TGGGAACTGATTCAAAACCTGACTAGAGTATGTAGAGGCTGTGAAATTTCTGT 663
 DB 550 TGGGAACTGATTCAAAACCTGACTAGAGTATGTAGAGGCTGTGAAATTTCTGT 609
 QY 664 GTAGCGGTAAATGTGCTAGTATTAAGAGGAAACCAAGTGGCGAAGCGACACTGAC 723
 DB 610 GTAGCGGTAAATGTGCTAGTATTAAGAGGAAACCAAGTGGCGAAGCGACACTGAC 669
 QY 724 TAATCTGACACTGAGTGTGCGAAGCTGTGGAGCAACAGATTAATACCTGTAGT 783
 DB 670 TAATCTGACACTGAGTGTGCGAAGCTGTGGAGCAACAGATTAATACCTGTAGT 729
 QY 784 CCAAGCGGTAAACGATGCACTAGCCGTTGGAACCTTGAAGCTTTAGTGGCGACCTA 843
 DB 730 CCAAGCGGTAAACGATGCACTAGCCGTTGGAAGCTTTGAAGCTTTAGTGGCGACCTA 789
 QY 844 ACGCATTAAGTGAACCGCTGGGAGTACGCGCCGCAAGGTTAAACTCAATGATTTAC 903
 DB 790 ACGCATTAAGTGAACCGCTGGGAGTACGCGCCGCAAGGTTAAACTCAATGATTTAC 849
 QY 904 GGGGCGCCGCAAGCGGTGAGCATGTGTTAATTGAAAGCAACCGAAGAACTTAC 963
 DB 850 GGGGCGCCGCAAGCGGTGAGCATGTGTTAATTGAAAGCAACCGAAGAACTTAC 909
 QY 964 CAGGCTTGAACATCAATGAATTTCTAGATATGATTTGGGCTTGGGAACTTGAGA 1023
 DB 910 CAGGCTTGAACATCAATGAATTTCTAGATATGATTTGGGCTTGGGAACTTGAGA 969
 QY 1024 CAGGCTTGAACATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1068
 DB 970 CAGGCTTGAACATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1014

Search completed: January 30, 2004, 19:20:12
 Job time : 319.06 secs


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QY 973 ACATCCATGAACTTTCTAGAGATAGATGTCCTCGGGAACATTGAGACAGGCTCTG 1032
Db 961 ACATGACAGAACTTTCCAGAGATGATGTCCTCGGGAACCTGACACAGGCTCTG 1020
QY 1033 CATGCTGCTGCTGAGCTGCTGTTGAAATGTAAG 1068
Db 1021 CATGCTGCTGCTGAGCTGCTGTTGAGATGTTGG 1056

RESULT 13
AAL50856
ID AAL50856 standard; DNA; 1480 BP.
AC AAL50856;
AL 30-JAN-2003 (first entry)
DE Benzene-degrading bacteria-related DNA sequence #2.
KM Benzene-degrading bacteria; benzene decomposition; ds.
XX Unidentified.
XX KR2002011252-A.
XX 08-FEB-2002.
XX 01-AUG-2000; 2000KR-0044629.
XX 01-AUG-2000; 2000KR-0044629.
XX (SMSU) SAMSUNG EVERLAND INC.
XX Park UH;
XX WPI; 2002-572306/61.
XX Benzene-degrading bacteria and its utilization method -
XX Dislosure; Fig 1; 7P; Korean.
XX The invention comprises a strain of bacteria (Pseudomonas putida) that is
XX useful for decomposing high concentrations of benzene (higher than
XX 1500ppm). The present DNA sequence is shown in a figure of the
XX specification.
SQ Sequence 1480 BP; 376 A; 330 C; 463 G; 311 T; 0 other;

Query Match 90.9%; Score 972.8; DB 24; Length 1480;
Best Local Similarity 95.1%; Pred. No. 1.2e-301;
Matches 1004; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 13 ATTGAACGCTGCGGCGAGCGCTTAACATGCAAGTCGAGCGGTAGAGAGAAGCTTGCTTC 72
Db 1 ATTGAACGCTGCGGCGAGCGCTTAACATGCAAGTCGAGCGGTAGAGAGAAGCTTGCTTC 60
QY 73 TCTTGAGAGCGCGGCGAGCGGTAGATGCTTGAATCTGCTGTAAGTGGGATTAAC 132
Db 61 TCGATTGCGGCGGCGAGCGGTAGATGCTTGAATCTGCTGTAAGTGGGATTAAC 120
QY 133 GTTCGAAACGAGCGCTAATACGATACGCTTCAAGGAGAAAGAGGGAACCTTCGGG 192
Db 121 GTTCGAAAGAGCGCTAATACGATACGCTTCAAGGAGAAAGAGGGAACCTTCGGG 180
QY 193 CCTTGCGCTATCAATAGAGCTTAGTGGATTGCTTAGTTGGTGAAGTAAAGCTTACCA 252
Db 181 CCTTGCGCTATCAATAGAGCTTAGTGGATTGCTTAGTTGGTGAAGTAAAGCTTACCA 240
QY 253 AGGCGAGATCCGTAATGCTGAGAGATGATCACTGGAACCTGAGACAGCT 312
Db 241 AGGCGAGATCCGTAATGCTGAGAGATGATCACTGGAACCTGAGACAGCT 300
QY 313 CCAAGCTCTTAGCGGAGGCGAGCTGCGGATTTGGACAAATGGCGAAAGCTTATCCA 372

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Db 301 CCAGACTCTTACGGGAGGCGAGCGTGGGAAATTTGGAACAATGGCGGAAAGCTTATCCA 360
QY 373 GCCATGCGCGGTGTGTAAGAAAGAGTCTTCGATTTGTAAGCACTTTAAGTGGAGAAAG 432
Db 361 GCCATGCGCGGTGTGTAAGAAAGTCTTCGATTTGTAAGCACTTTAAGTGGAGAAAG 420
QY 433 GGTGTAGATTAATCTCTGCAATTTTGAAGTTCACGACAAATAGACACCGGCTAATC 492
Db 421 GGCATTACCTTAATAGATGATGTTTGAAGTTCACGACAAATAGACACCGGCTAATC 480
QY 493 TGTGCGACGACCGCGTAAATACAGAGGAGTGAAGGCTTAATGGAATTAATCTGAGGCTTA 552
Db 481 TGTGCGACGACCGCGGTAAATACAGAGGAGTGAAGGCTTAATGGAATTAATCTGAGGCTTA 540
QY 553 AGCGCGGAGTGGTGTGTTTGAAGTGAATGCCCGGCTCAACCTGAGAACTG 612
Db 541 AGCGCGGAGTGGTGTGTTTGAAGTGAATGCCCGGCTCAACCTGAGAACTG 600
QY 613 CATTCAAACTGACTGATAGATAGTGAAGGAGTGAATTTCTGTTAGCGGTG 672
Db 601 CATTCAAACTGACTGATAGATAGTGAAGGAGTGAATTTCTGTTAGCGGTG 660
QY 673 AATGCGTAGATATAGAGAGAAACACAGTGGCGAAGCGCACCTGACTAATATCTGA 732
Db 661 AATGCGTAGATATAGAGAGAAACACAGTGGCGAAGCGCACCTGACTAATATCTGA 720
QY 733 CACTGAGTGGCGAAGCGTGGAGAGCAACAGATTAATACCTGTTAGTTCACGCCGT 792
Db 721 CACTGAGTGGCGAAGCGTGGAGAGCAACAGATTAATACCTGTTAGTTCACGCCGT 780
QY 793 AAAGATGCTAATGACCTGTTGAAGCTTTAGTGAAGCTTTAGTGGCCAGCTAAGCATTA 852
Db 781 AAAGATGCTAATGACCTGTTGAAGCTTTAGTGAAGCTTTAGTGGCCAGCTAAGCATTA 840
QY 853 GTTGACCGCTGGGAGTACGCGCCGAGCTTAAACTCAATGATTAAGCGGCGCG 912
Db 841 GTTGACCGCTGGGAGTACGCGCCGAGCTTAAACTCAATGATTAAGCGGCGCG 900
QY 913 CACAGCGGTGAGCATGATGTTTAATTGAGAGCAACGCGAATTAACCTTACAGGCCCTG 972
Db 901 CACAGCGGTGAGCATGATGTTTAATTGAGAGCAACGCGAATTAACCTTACAGGCCCTG 960
QY 973 ACATCCATGAACTTTCTAGAGATAGATGTCCTTGGGAACATGAGACAGGTGCTG 1032
Db 961 ACATCCAGAGAACTTCCAGAGATGATGTCCTTGGGAACATGAGACAGGTGCTG 1020
QY 1033 CATGCTGCTGCTGAGCTGCTGTTGAAATGTAAG 1068
Db 1021 CATGCTGCTGCTGAGCTGCTGTTGAGATGTTGG 1056

RESULT 14
AAT18764
ID AAT18764 standard; rRNA; 1518 BP.
AC AAT18764;
AL 05-JUL-1996 (first entry)
DE Pseudomonas aeruginosa 16S ribosomal RNA.
KM Atrazine; pesticide degradation; soil decontamination;
KM bioremediation; s-triazine; herbicide; ss.
XX Pseudomonas aeruginosa.
XX OS
XX FH
FH Key Location/Qualifiers
FT misc_difference 46
FT /note "base 46 is identified as 'n'"
FT misc_difference 221
FT /tag= b

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CC compatible, functional polymers, such as device materials and soft
 CC medical materials. The present sequence represents the basic nucleotide
 CC sequence of 16S rRNA of *P. jessenii* strain Pl61, a microorganism isolated
 CC from soil that can produce PHAs.

XX Sequence 1501 BP; 379 A; 339 C; 475 G; 308 T; 0 other;

Query Match 92.1%; Score 985.2; DB 24; Length 1501;

Best Local Similarity 95.9%; Pred. No. 1.3e-305;

Matches 1011; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

```

QY 15 TGAAGCTGGGGGCGGCGCTTAACATGCGAGGTGAGAGAGAGCTTCTC 74
DB 1 TGAAGCTGGGGGCGGCGCTTAACATGCGAGGTGAGAGAGAGCTTCTC 60
QY 75 TTGAAGCGGCGGAGCGGCTGAGTAATGCTTAGAACTGCTGTAGTGGGGATTA 134
DB 61 AATTGACGCGCGGAGCGGCTGAGTAATGCTTAGAACTGCTGTAGTGGGGATTA 120
QY 135 TGGGAAACGAGCGCTTAATCCGCAATGCTTACGCGGAGAAAGAGCGGCGCTT 134
DB 121 CTGAAAGGAGCGCTTAATCCGCAATGCTTACGCGGAGAAAGAGCGGCGCTT 180
QY 195 TTGCGCTATCAGATGAGCGCTAGGTGAGTAATGCTAGTGTGAGGTAAATGCT 254
DB 181 TTGCGCTATCAGATGAGCGCTAGGTGAGTAATGCTAGTGTGAGGTAAATGCT 240
QY 255 GCGACGATCCGTAATCTGCTGAGAGATGATCACTGCACTGCACTGAGACAGCT 314
DB 241 GCGACGATCCGTAATCTGCTGAGAGATGATCACTGCACTGCACTGAGACAGCT 300
QY 315 AGACTCTCAGGAGGAGCGAGCACTGAGGAAATTTGACATAGGCGAAAGCTGAT 374
DB 301 AGACTCTCAGGAGGAGCGAGCACTGAGGAAATTTGACATAGGCGAAAGCTGAT 360
QY 375 CATGCCGCTGTGTGAAGAAGGCTTCGAGTTGAACCACTTTAAGTGGAGAGAG 434
DB 361 CATGCCGCTGTGTGAAGAAGGCTTCGAGTTGAACCACTTTAAGTGGAGAGAG 420
QY 435 TTGTAGATTAATCTCTGCAATTTTGAAGTACCGAGAGATTAACCGCGCTACT 494
DB 421 CATTAACCTTAATCTCTGCAATTTTGAAGTACCGAGAGATTAACCGCGCTACT 480
QY 495 TGCACAGCAGCGCGGTAATACAGAGGCTGCAAGCTTAATCGGAATTAAGT 554
DB 481 TGCACAGCAGCGCGGTAATACAGAGGCTGCAAGCTTAATCGGAATTAAGT 540
QY 555 CGGCGCTAGTGTGTGAAGAAGGCTTCGAGTTGAACCACTTTAAGTGGAGAG 614
DB 541 CGGCGCTAGTGTGTGAAGAAGGCTTCGAGTTGAACCACTTTAAGTGGAGAG 600
QY 615 TTCAAAACTGACTGACTAGATGATGAGAGGCTGAGGAAATTTCTGTGAGCGT 674
DB 601 TTCAAAACTGACTGACTAGATGATGAGAGGCTGAGGAAATTTCTGTGAGCGT 660
QY 675 ATGCGTAATATGAGAGAGAAACAGAGTGGCGAAGCGCACTGAGCTAATCT 734
DB 661 ATGCGTAATATGAGAGAGAAACAGAGTGGCGAAGCGCACTGAGCTAATCT 720
QY 735 CTGAGGTGCGAAAGCGTGGGAGCAAAACAGATTGATACCTGGTAGTCCAC 794
DB 721 CTGAGGTGCGAAAGCGTGGGAGCAAAACAGATTGATACCTGGTAGTCCAC 780
QY 795 AGGATGTCACTAGCGCTTGAAGCGCTTTAGTGGCGCACTGAAGCTTAAGT 854
DB 781 AGGATGTCACTAGCGCTTGAAGCGCTTTAGTGGCGCACTGAAGCTTAAGT 840
QY 855 TGAACGCTGCGGAGAGTACGCGCAAGGTTAAATCTCAATTAATGAGCGGCG 914
DB 841 TGAACGCTGCGGAGAGTACGCGCAAGGTTAAATCTCAATTAATGAGCGGCG 900
QY 915 CAAGCGGTGAGAGATGTGTTAATTCGAGAGCAAGCAACCTTACAGGCTTGAC 974

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DB 901 CAAGCGGTGAGAGATGTGTTAATTCGAGAGCAACCGAAGAACTTACAGGCTTAC 960
QY 975 ATCCATGAACTTTCTAGATGATGATGCTGCTTGGGAAACATTGAGACAGTGTGCA 1034
DB 961 ATCCATGAACTTTCTAGATGATGATGCTGCTTGGGAAACATTGAGACAGTGTGCA 1020
QY 1035 TGGCTGTGCTAGCTGCTGTGTGAATGTAAAG 1068
DB 1021 TGGCTGTGCTAGCTGCTGTGTGAATGTAAAG 1054

```

RESULT 10

AA166302 standard; DNA; 1501 BP.

AA166302;

22-JAN-2002 (first entry)

Pseudomonas jessenii coding sequence.

Polyhydroxyalkanoate; 3-hydroxythienylalkanoic acid; PHA;

medical material; biodegradable polymer; ds.

Pseudomonas jessenii.

EP130043-A2.

05-SEP-2001.

28-FEB-2001; 2001EP-0104922.

29-FEB-2000; 2000JP-0054317.

29-FEB-2000; 2000JP-0054667.

(CANO) CANON KK.

Horna T, Yano T, Kobayashi S, Imamura T, Kenmoku T, Kozaki S;

WPI; 2002-012494/02.

Novel polyhydroxy alkanates containing 3-hydroxy thienyl alkanolic acid

monomer units for use as biodegradable and functional polymers -

Disclosure; Page 32-33; 46p; English.

The present invention relates to polyhydroxy alkanates (PHA) containing

3-hydroxy thienyl alkanolic acid monomer units. These can be used as

biodegradable, bio-compatible, functional polymers, as device material

and as soft medical material. The present sequence is a coding sequence

from *Pseudomonas jessenii*.

Sequence 1501 BP; 379 A; 339 C; 475 G; 308 T; 0 other;

Query Match 92.1%; Score 985.2; DB 24; Length 1501;

Best Local Similarity 95.9%; Pred. No. 1.3e-305;

Matches 1011; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

```

QY 15 TGAAGCTGGGGGCGGCGCTTAACATGCGAGGTGAGAGAGCTTCTC 74
DB 1 TGAAGCTGGGGGCGGCGCTTAACATGCGAGGTGAGAGAGCTTCTC 60
QY 75 TTGAAGCGGCGGAGCGGCTGAGTAATGCTTAGAACTGCTGTAGTGGGGATTA 134
DB 61 AATTGACGCGCGGAGCGGCTGAGTAATGCTTAGAACTGCTGTAGTGGGGATTA 120
QY 135 TGGGAAACGAGCGCTTAATCCGCAATGCTTACGCGGAGAAAGAGCGGCGCTT 194
DB 121 CTGAAAGGAGCGCTTAATCCGCAATGCTTACGCGGAGAAAGAGCGGCGCTT 180
QY 195 TTGCGCTATCAGATGAGCGCTAGTGTGAGTAATGCTAGTGTGAGTAATGCT 254
DB 181 TTGCGCTATCAGATGAGCGCTAGTGTGAGTAATGCTAGTGTGAGTAATGCT 240

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PF	27-DEC-2000;	2000EP-0128540.	
XX			
PR	27-DEC-1999;	99JP-0371864	
PR	27-DEC-1999;	99JP-0371867	
PR	27-DEC-1999;	99JP-0371868	
PR	27-DEC-1999;	99JP-0371869	
PR	31-JAN-2000;	2000JP-0023024	
PR	31-JAN-2000;	2000JP-0023025	
PR	28-NOV-2000;	2000JP-0361323.	
XX			
PA	(CANO)	CANON KK.	
PI	Honma T, Kobayashi T, Yano T, Kobayashi S, Imamura T, Suda S;		
PI	Kenmoku T;		
XX			
DR	WPI; 2001-598513/68.		
PT	Polyhydroxyalkanoate comprises monomeric unit that has pendant		
PS	alkylaryl group, optionally substituted on benzene ring.		
XX			
XX	Disclosure; Fig 12; 95pp; English.		
CC	The present sequence represents that of the 16S rRNA (ribosomal RNA) gene		
CC	from <i>Pseudomonas jesseni</i> strain 161. Prior to the present invention,		
CC	strain 161 had not been assigned to a particular species; comparison		
CC	of the strain 161 16S rRNA gene DNA with 16S rRNA gene sequences of		
CC	known micro-organisms of the genus <i>Pseudomonas</i> identified 161 as a		
CC	strain of <i>Pseudomonas jesseni</i> . The specification describes a		
CC	polyhydroxyalkanoate comprising one or more monomeric units that have		
CC	pendant alkylaryl groups, optionally substituted on the benzene ring.		
CC	The specification also describes a process of producing the		
CC	polyhydroxyalkanoate by culturing a micro-organism in a medium containing		
CC	a raw material alkanoate and a yeast extract so that the alkanoate is		
CC	polymerised. The invention is used for the production of novel		
CC	polyalkanoates using microbial enzymes. The polymer is adhesive at		
CC	ambient temperatures and, when mixed with other polymers, reduces the		
CC	glass transition temperature of the blend. Orientation and crystallinity		
CC	can be tailored by changing the pendant substituent groups. The desired		
CC	polymer can be obtained without interference from unintended monomer		
XX	units.		
XX			
XX	Sequence 1501 BP; 379 A; 339 C; 475 G; 308 T; 0 other;		
SQL			
Query Match	92.1%;	Score 985.2;	DB 23; Length 1501;
Best Local Similarity	95.9%;	Pred. No. 1.3e-305;	
Matches 101;	Conservative 0;	Mismatches 43;	Indels 0; Gaps 0
QY	15 TGAAGCCTGGCGGCGAGCCCTTAACAATCAATCAAGTGGAGGATAGAGAAAGCTTGCTTC	74	
DB	1 TGAAGCCTGGCGGCGAGCCCTTAACAATCAATCAAGTGGAGGATAGAGAAAGCTTGCTTC	60	
QY	75 TTGAGAGCGGCGGAGCGGATTAATGCTTGAGGAAATCGCTGCTATGAGGGATAAAGT	134	
DB	61 AATTCAGCGCGGAGCGGATTAATGCTTGAGGAAATCGCTGCTATGAGGGATAAAGT	120	
QY	135 TCGGAAGCGAGCGCTAATACCGCATACGCTCTTACGGGAGAAAGCAGGGAGACTTGGGGCC	194	
DB	121 CTGGAAGGAGCGCTAATACCGCATACGCTCTTACGGGAGAAAGCAGGGAGACTTGGGGCC	180	
QY	195 TTGCGGTATCAGATGAGGCTTAGTGGATTAAGCTAGTTGGTGGAGCTAATGGCTCACAG	254	
DB	181 TTGCGGTATCAGATGAGGCTTAGTGGATTAAGCTAGTTGGTGGAGCTAATGGCTCACAG	240	
QY	255 GCGAGCATCCGTAATCTGATCTTGAGAGATGATCAAGTCAACTGGAACCTGAGACAGGATCC	314	
DB	241 GCGAGCATCCGTAATCTGATCTTGAGAGATGATCAAGTCAACTGGAACCTGAGACAGGATCC	300	
QY	315 AGACTCTCTACGGGAGGAGCAGTGGGAAATTTGGAGCAATGGGAGAAAGCTTATCCAG	374	
DB	301 AGACTCTCTACGGGAGGAGCAGTGGGAAATTTGGAGCAATGGGAGAAAGCTTATCCAG	360	
QY	375 CATGCCGCTGTGTGAAGAGGTCTTGCGATTGTAAAGCACTTTAATTGGAGGAAAGG	434	

Db	361	CATGCCGCGTGTGTGAAAGAGTCTTTCGAGATTGTAAGCACTTTAAGTTGGAGGAAAGG	420
Qy	435	TGTGATTAATATACCTCGCAATTTTGACGATTAACGACAGAAATTAAGCACCGGATACCTG	494
Db	421	CATTAACTTAATACCTTAGTGTGTTTGACGTTACCGACAGAAATTAAGCACCGGCTAACTG	480
Qy	495	TGCGACAGACCGCGGTAAATACAGAGGGTGCAGCGTTAATCGGAATTACTGGGCGTAAAG	554
Db	481	TGCGACAGACCGCGGTAAATACAGAGGGTGCAGCGTTAATCGGAATTACTGGGCGTAAAG	540
Qy	555	CGCGGTAGGCGTGTGTTGTTAGTTGAGATGGAATCCCCGGGGCTCAACTGGGAACTGCA	614
Db	541	CGCGGTAGGCGTGTGTTGTTAGTTGAGATGGAATCCCCGGGGCTCAACTGGGAACTGCA	600
Qy	615	TTCCAAACTGACTGACTAGATATGTAGAGGGTGTGGAATTTCTGTGTAGCGGTGA	674
Db	601	TTCCAAACTGACTGACTAGATATGTAGAGGGTGTGGAATTTCTGTGTAGCGGTGA	660
Qy	675	ATGCGTAGATATAGGAAGAAACACAGATGGCGAAGGCGACACCTGGAATTAATCTGACA	734
Db	661	ATGCGTAGATATAGGAAGAAACACAGATGGCGAAGGCGACACCTGGAATTAATCTGACA	720
Qy	735	CTGAGGTGCGAAAGCGTGGGAGCGAAACAGAGATTAGATACCCTGTGTAGTCCAGCCGTGA	794
Db	721	CTGAGGTGCGAAAGCGTGGGAGCGAAACAGAGATTAGATACCCTGTGTAGTCCAGCCGTGA	780
Qy	795	ACGATGTCACTAGACCGGTGGAAACCTTGAGCTTTTAGTGGCGCAGCTAAACGCTTAAGT	854
Db	781	ACGATGTCACTAGACCGGTGGAAACCTTGAGCTTTTAGTGGCGCAGCTAAACGCTTAAGT	840
Qy	855	TGACCGCCTGGGAGATACGCGCCGCAAGATTAAACTCTCAATGAATGACCGGCGGCCGCA	914
Db	841	TGACCGCCTGGGAGATACGCGCCGCAAGATTAAACTCTCAATGAATGACCGGCGGCCGCA	900
Qy	915	CAAGCGGTAGAGCATATGTGTTAATTTGAGAGCAACGCGAAACCTTAACAGGCGCTTGAC	974
Db	901	CAAGCGGTAGAGCATATGTGTTAATTTGAGAGCAACGCGAAACCTTAACAGGCGCTTGAC	960
Qy	975	ATCCAAATGAATTTCTAGAGATAGATTGTGCTTCGGGAAACATTGAGACAGGTGCTGCA	1034
Db	961	ATCCAAATGAATTTCTAGAGATAGATTGTGCTTCGGGAAACATTGAGACAGGTGCTGCA	1020
Qy	1035	TGCGTGTGCTGACGTCGATGTTGTGAATGTAAAG	1068
Db	1021	TGCGTGTGCTGACGTCGATGTTGTGAATGTAAAG	1054
RESULT 8			
AAL39554			
ID	AAL39554	standard; DNA; 1501 BP.	
XX	AAL39554;		
AC	AAL39554;		
DT	05-SEP-2002 (first entry)		
XX			
DE	Pseudomonas jessenii Pl61 strain DNA.		
XX			
KW	Polyhydroxyalkanoate; PHA; benzoyl alkanolic acid; device material;		
XX	water repellent; medical material; Pseudomonas jessenii; Pl61 strain; ds.		
XX	Pseudomonas jessenii.		
CS			
FN	EP188782-A2.		
XX			
PD	20-MAR-2002.		
XX			
PF	14-SEP-2001; 2001EP-0122101.		
XX			
ER	14-SEP-2000; 2000JP-0279900.		
ER	13-DEC-2000; 2000JP-0378827.		
ER	31-MAY-2001; 2001JP-0165238.		
ER	31-MAY-2001; 2001JP-0165509.		

QY 735 CTGAGGTGCGAAAGCTGGGGAGCAACAGATTAGATACCTGTTAGTCCACCCGTAA 794
DB 721 CTGAGGTGCGAAAGCTGGGGAGCAACAGATTAGATACCTGTTAGTCCACCCGTAA 780
QY 795 ACGATGTCAACTAGCCGTTGGAGAGCCTTTAGTGGCGCAGCTAACGACTTAAGT 854
DB 781 ACGATGTCAACTAGCCGTTGGAGAGCCTTTAGTGGCGCAGCTAACGACTTAAGT 840
QY 855 TGACCGCTGGGGAGTACGGCCGCAAGGTTAAACTCAATGAATGACGGGGGCGCGCA 914
DB 841 TGACCGCTGGGGAGTACGGCCGCAAGGTTAAACTCAATGAATGACGGGGGCGCGCA 900
QY 915 CAAGCGGTGAGCATGTGTTTAATTGAGAGCAAGCGAGAACTTACAGGCTTGGAC 974
DB 901 CAAGCGGTGAGCATGTGTTTAATTGAGAGCAAGCGAGAACTTACAGGCTTGGAC 960
QY 975 ATCCAAATGAACCTTTCTAGAGATAGATGTGCTGCTTGGAGAACTTGAAGAGGTGCTGCA 1034
DB 961 ATCCAAATGAACCTTTCTAGAGATAGATGTGCTGCTTGGAGAACTTGAAGAGGTGCTGCA 1020
QY 1035 TGCGTGTGCTGAGCTGCTGTTGTAATGTAAG 1068
DB 1021 TGCGTGTGCTGAGCTGCTGTTGTAATGTAAG 1054

RESULT 5

AAH77497
ID AAH77497 standard; DNA; 1501 BP.

XX AAH77497;

DT 20-NOV-2001 (first entry)

DE Pseudomonas jessenii p161 coding sequence fragment.

KM Polyhydroxyalkanoate; PHA; ds.

OS Pseudomonas jessenii.

PN JP2001178485-A.

PD 03-JUL-2001.

PF 27-DEC-1999; 99JP-0371865.

PR 27-DEC-1999; 99JP-0371865.

PA (CANO) CANON KK.

DR WPI; 2001-586288/66.

PT Production of a polyhydroxyalkanoate useful as a functional polymer -

PS Disclosure; Page 9; 12pp; Japanese.

XX The present invention describes a method of producing a
CC polyhydroxyalkanoate (PHA) using a microbe. This may be Pseudomonas
CC chloridi YN3, Pseudomonas chloridi H45 or Pseudomonas jessenii P161. The
CC PHA produced using the method of the invention is useful as a functional
CC polymer. The present sequence is a fragment of the P. jessenii coding
CC sequence.

SQ Sequence 1501 BP; 379 A; 339 C; 475 G; 308 T; 0 other;

Query Match 92.1%; Score 985.2; DB 22; Length 1501;

Best Local Similarity 95.9%; Pred. No. 1.3e-305;

Matches 1011; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 15 TGAACGCTGCGGAGAGCTTAACATGCAAGTCGAGCGTGAAGAGAGCTTGTCTC 74
DB 1 TGAACGCTGCGGAGAGCTTAACATGCAAGTCGAGCGTGAAGAGAGCTTGTCTC 60
QY 75 TTGAGAGCGGAGAGCGGTGAGTATGCTTAGGAATTCGCTGTGATGAGGAGTAACGT 134

DB 61 AATTGAGCGGCGAGAGGCTGAGTATGCTTAGGAATTCGCTGTTAGTGGGAGCAACGT 120
QY 135 TGGGAAAGGAGAGCTTAACATGCAAGTCGAGCGTGAAGAGAGCTTGTCTC 134
DB 121 CTGGAAGGAGAGCTTAACATGCAAGTCGAGCGTGAAGAGAGCTTGTCTC 180
QY 195 TTGCGCTACATGATGAGCTAGTCCGATTTAGTGTGATGAGTAAATGCTACCAAG 254
DB 181 TTGCGCTACATGATGAGCTAGTCCGATTTAGTGTGATGAGTAAATGCTACCAAG 240
QY 255 GCGAGATCCGTAATGCTGTAAGAGATGATCACTGCACTGGAATGAGACAGCTTCC 314
DB 241 GCGAGATCCGTAATGCTGTAAGAGATGATCACTGCACTGGAATGAGACAGCTTCC 300
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DB 301 AGACTCTTACGAGGAGGAGAGCTGAGGAGAAATTGAGCAATGAGGAGGAGCTGATCAGC 360
QY 375 CATGCCGCTGTGTGAGAGAGCTTCCGATTTGTAAGCACTTAACTTGGAGGAGAGG 434
DB 361 CATGCCGCTGTGTGAGAGAGCTTCCGATTTGTAAGCACTTAACTTGGAGGAGAGG 420
QY 435 TTGTAATTAATACCTGCAATTTTGAAGTGAACCTGACAGCAAGTAAGCAAGGCTAACCTG 434
DB 421 CATTAACCTTAATACCTGCAATTTTGAAGTGAACCTGACAGCAAGTAAGCAAGGCTAACCTG 480
QY 495 TGCCAGAGAGCGCGGTATATACAGAGGAGTCAAGGCTTAATCGAATTAAGCGGTAAAG 554
DB 481 TGCCAGAGAGCGCGGTATATACAGAGGAGTCAAGGCTTAATCGAATTAAGCGGTAAAG 540
QY 555 CCGCGGTAGGTGTTTGTAAAGTGTGAATTCGCCGAGCTCAACCTTGGAGACTGCA 614
DB 541 CCGCGGTAGGTGTTTGTAAAGTGTGAATTCGCCGAGCTCAACCTTGGAGACTGCA 600
QY 615 TTCAAACTGACTGCTAGAGATAGGTGAGAGGAGTGTGGAATTCCTGTAGGAGGAGAA 674
DB 601 TTCAAACTGACTGCTAGAGATAGGTGAGAGGAGTGTGGAATTCCTGTAGGAGGAGAA 660
QY 675 ATGCGTATATAGAGAGAGAACCAAGTGGAGAGGAGGAGCACTGAGCTAATTAAGTACA 734
DB 661 ATGCGTATATAGAGAGAGAACCAAGTGGAGAGGAGGAGCACTGAGCTAATTAAGTACA 720
QY 735 CTGAGGTGCGAAAGCTGGGGAGCAACAGATTAGATACCTGTTAGTCCACCCGTAA 794
DB 721 CTGAGGTGCGAAAGCTGGGGAGCAACAGATTAGATACCTGTTAGTCCACCCGTAA 780
QY 795 ACGATGTCAACTAGCCGTTGGAGAGCCTTTAGTGGCGCAGCTAACGACTTAAGT 854
DB 781 ACGATGTCAACTAGCCGTTGGAGAGCCTTTAGTGGCGCAGCTAACGACTTAAGT 840
QY 855 TGACCGCTGGGGAGTACGGCCGCAAGGTTAAACTCAATGAATGACGGGGGCGCGCA 914
DB 841 TGACCGCTGGGGAGTACGGCCGCAAGGTTAAACTCAATGAATGACGGGGGCGCGCA 900
QY 915 CAAGCGGTGAGCATGTGTTTAATTGAGAGCAAGCGAGAACTTACAGGCTTGGAC 974
DB 901 CAAGCGGTGAGCATGTGTTTAATTGAGAGCAAGCGAGAACTTACAGGCTTGGAC 960
QY 975 ATCCAAATGAACCTTTCTAGAGATAGATGTGCTGCTTGGAGAACTTGAAGAGGTGCTGCA 1034
DB 961 ATCCAAATGAACCTTTCTAGAGATAGATGTGCTGCTTGGAGAACTTGAAGAGGTGCTGCA 1020
QY 1035 TGCGTGTGCTGAGCTGCTGTTGTAATGTAAG 1068
DB 1021 TGCGTGTGCTGAGCTGCTGTTGTAATGTAAG 1054

RESULT 6

AAH77497
ID AAH77497 standard; DNA; 1501 BP.

XX AAH77497;

```

Db      241 GCGACGATCGTAACTGATCTGAGGAGTGAATGATCACTGAGAACTGAGACACGGCTCC 300
Qy      315 AGACTCTACGGGAGGACAGCAGTGGGGAATATTGACATATGGCGAAAGCCTGATCCAG 374
Db      301 AGACTCTACGGGAGGACAGCAGTGGGGAATATTGACATATGGCGAAAGCCTGATCCAG 360
Qy      375 CATGCCGCTGTGTATAAGAGTCTTCGGATTTGTAAGCACTTAATTGGGAGGAAGG 434
Db      361 CATGCCGCTGTGTATAAGAGTCTTCGGATTTGTAAGCACTTAATTGGGAGGAAGG 420
Qy      435 TTGTAGATTAACTCTGCAATTTTGAAGTACCGAGAGATAGCAACCGGCTAATCTG 494
Db      421 CATTAACCTAATAGCTTAGTGTGTTGAGCTTACCGAGAGATAGCAACCGGCTAATCTG 480
Qy      495 TCCCGACAGCCCGGTAATACAGAGGTGCAAGGTTAATCGAATTACTGGCGTAAAG 554
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Qy      555 CCGCGGTAGTGTGTGTTAAGTGTGATGTAATCCCGGCTCAACTGGGACTGCA 614
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Qy      615 TTCAAACTGACTGACTAGATATGTATGAGCGGTGTGGAATTTCTGTGTAGCGGTGA 674
Db      601 TTCAAACTGACTGACTAGATATGTATGAGCGGTGTGGAATTTCTGTGTAGCGGTGA 660
Qy      675 ATGGGTAGATATAGGAAGAAACACAGTGGCGAAGGAGCACTCGGCTAATAGTACA 734
Db      661 ATGGGTAGATATAGGAAGAAACACAGTGGCGAAGGAGCACTCGGCTAATAGTACA 720
Qy      725 CTGAGGTGCGAAAGCGTGGGAGCAACAGGATTAATACCTGTAGTCAAGCCGTAA 794
Db      721 CTGAGGTGCGAAAGCGTGGGAGCAACAGGATTAATACCTGTAGTCAAGCCGTAA 780
Qy      795 ACGATGCACTAGCCGTTGGAACCTTTAGCTTTAGTGGCGGAGTAACTGAATAGT 854
Db      781 ACGATGCACTAGCCGTTGGAACCTTTAGCTTTAGTGGCGGAGTAACTGAATAGT 840
Qy      855 TGACCGCTGCGGAGTACGCGCGCAAGGTTAAATCAATTAATGAATGACGGGCGCCGA 914
Db      841 TGACCGCTGCGGAGTACGCGCGCAAGGTTAAATCAATTAATGAATGACGGGCGCCGA 900
Qy      915 CAAAGGCTGAGCATGTGTGTTAATTGAAAGCAACGGCAACCTTAACAGGCTTGA 974
Db      901 CAAAGGCTGAGCATGTGTGTTAATTGAAAGCAACGGCAACCTTAACAGGCTTGA 960
Qy      975 ATCCATGAACCTTTCTAGATATGATGATGATGATGATGATGATGATGATGATG 1034
Db      961 ATCCATGAACCTTTCTAGATATGATGATGATGATGATGATGATGATGATGATG 1020
Qy      1035 TGGCTGTGCTAGCTCGTGTGTGAATGTAAG 1068
Db      1021 TGGCTGTGCTAGCTCGTGTGTGAATGTAAG 1054

```

RESULT 4

AA164998

ID AA164998 standard; DNA; 1501 BP.

AA164998;

11-DEC-2001 (first entry)

DE Polyhydroxyalkanoic acid related Pseudomonas jessenii coding sequence.

XX Polyhydroxyalkanoic acid; PHA; biodegradable plastic; ds.

XX Pseudomonas jessenii.

XX JP2001178464-A.

XX 03-JUL-2001.

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XX      27-DEC-1999; 99JP-0371866.
XX      27-DEC-1999; 99JP-0371866.
XX      (CANO ) CANON KK.
XX      WPT: 2001-592589/67.
XX      Microbial preparation of polyhydroxyalkanoic acids, using new carbon
XX      sources useful as raw material for biodegradable plastics -
XX      Disclosure; Page 9; 10pp; Japanese.
XX      The present invention relates to the production of
XX      polyhydroxyalkanoic acids. These can then be used in the production of
XX      biodegradable plastics. The present sequence is a Pseudomonas jessenii
XX      coding sequence described in the exemplification of the invention.
XX      Sequence 1501 BP; 379 A; 339 C; 475 G; 308 T; 0 other;

```

Query Match 92.1%; Score 985.2; DB 22; Length 1501;
Best Local Similarity 95.9%; Pred. No. 1,3e-305;
Matches 1011; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

```

Qy      15 TGAACGCTGCGGAGGCTTAACATGACATGACAGCGGTAGAGGAAGCTTGCTCTC 74
Db      1 TGAACGCTGCGGAGGCTTAACATGACATGACAGCGGTAGAGGAAGCTTGCTCTC 60
Qy      75 TTGAGAGCGCGGAGCGGTGAGTAATGCTTAGAATCTGCTGTAGTGGGAGTAACTG 134
Db      61 AATTACACCGCGGAGCGGTGAGTAATGCTTAGAATCTGCTGTAGTGGGAGTAACTG 120
Qy      135 TCGGAACGAGACGCTAATACCGCATACGCTTACGCGGAGGAAGCAAGGAGCCTTGCGGCC 194
Db      121 CTGGAAGGAGACGCTAATACCGCATACGCTTACGCGGAGGAAGCAAGGAGCCTTGCGGCC 180
Qy      195 TTGGCTATCAGATGAGCCTAGTCCGATTAAGTATGATGATGATGATGATGATGATG 254
Db      181 TTGGCTATCAGATGAGCCTAGTCCGATTAAGTATGATGATGATGATGATGATGATG 240
Qy      255 GCGACGATCCGCTAATGCTGTGAGAGATGATGATGATGATGATGATGATGATGATG 314
Db      241 GCGACGATCCGCTAATGCTGTGAGAGATGATGATGATGATGATGATGATGATGATG 300
Qy      315 AGACTCTACGGGAGGACAGCAGTGGGGAATTTGACATATGGCGAAAGCCTGATCCAG 374
Db      301 AGACTCTACGGGAGGACAGCAGTGGGGAATTTGACATATGGCGAAAGCCTGATCCAG 360
Qy      375 CATGCCGCTGTGTATAAGAGTCTTCGGATTTGTAAGCACTTAATTGGGAGGAAGG 434
Db      361 CATGCCGCTGTGTATAAGAGTCTTCGGATTTGTAAGCACTTAATTGGGAGGAAGG 420
Qy      435 TTGTAGATTAACTCTGCAATTTTGAAGTACCGAGAGATAGCAACCGGCTAATCTG 494
Db      421 CATTAACCTAATAGCTTAGTGTGTTGAGCTTACCGAGAGATAGCAACCGGCTAATCTG 480
Qy      495 TCCCGACAGCCCGGTAATACAGAGGTGCAAGGTTAATCGAATTACTGGCGTAAAG 554
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Db      541 CCGCGGTAGTGTGTGTTAAGTGTGATGTAATCCCGGCTCAACTGGGAGTGA 600
Qy      615 TTCAAACTGACTGACTAGATATGTATGAGCGGTGTGGAATTTCTGTGTAGCGGTGA 674
Db      601 TTCAAACTGACTGACTAGATATGTATGAGCGGTGTGGAATTTCTGTGTAGCGGTGA 660
Qy      675 ATGGGTAGATATAGGAAGAAACACAGTGGCGAAGGAGCAACCTGAGCTAATAGTACA 734
Db      661 ATGGGTAGATATAGGAAGAAACACAGTGGCGAAGGAGCAACCTGAGCTAATAGTACA 720

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PT Preparing anti-freeze peptides useful in frozen food products, e.g.
 PT frozen vegetables and confectionery, by culturing bacteria from aqueous
 PT low-temperature environment and extracting anti-freeze proteins from
 PT culture

XX Claim 3, Page 56, 59pp; English.

CC The present sequence represents the 16S rRNA of *Pseudomonas* sp.
 CC isolate 20. Anti-freeze proteins can be isolated from *Pseudomonas* sp.,
 CC using the method of the invention. The specification describes a method
 CC for producing anti-freeze peptides (AFPs). The method comprises
 CC collecting one or more samples of bacteria from an aqueous
 CC low-temperature environment, culturing the bacteria and extracting
 CC proteins from the samples, testing the proteins for anti-freeze
 CC properties, selecting proteins having anti-freeze properties and
 CC producing the selected protein for use as an AFP food additive. The
 CC method is useful for producing AFPs which are incorporated in food
 CC products, such as frozen vegetables and frozen confectionery such as
 CC ice-cream. AFPs are useful in frozen food products, such as vegetables,
 CC sauces, soups, snacks, dairy products and frozen confectionery, which
 CC includes sorbet, water-ice, granites, frozen fruit purees and
 CC milk-containing frozen products such as ice-cream, frozen yogurt or
 CC custards, sherbet and ice-milk.

SQ Sequence 1070 BP, 280 A, 223 C, 336 G, 231 T, 0 other;

Query Match 100.0%; Score 1070; DB 22; Length 1070;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1070; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCCTTGCTGATGAAACGCTGGCGGAGCCTTAACACATGCAAGTCAAGCGGTAGAGA 60
 DB 1 GCCCTTGCTGATGAAACGCTGGCGGAGCCTTAACACATGCAAGTCAAGCGGTAGAGA 60
 QY 61 GAAGCTTGCTCTCTTGAAGCGCGGAGCGGTAGATGCTAGAAATCTGCTGGGTA 120
 DB 61 GAAGCTTGCTCTCTTGAAGCGCGGAGCGGTAGATGCTAGAAATCTGCTGGGTA 120
 QY 121 GTGGGGGATTAAGTTCGAAAACGACGCTTAATACCGATACGCTCTCAACGCGGAAAACG 180
 DB 121 GTGGGGGATTAAGTTCGAAAACGACGCTTAATACCGATACGCTCTCAACGCGGAAAACG 180
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 QY 241 AATGCTTCACCAAGGCGACGATCGTACTGCTGAGAGATGATCACTGGA 300
 DB 241 AATGCTTCACCAAGGCGACGATCGTACTGCTGAGAGATGATCACTGGA 300
 QY 301 CTGAGACACGCTCCAGCTCTGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
 DB 301 CTGAGACACGCTCCAGCTCTGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
 QY 361 AAGCTGATCCAGCCATGCGCGGTGTGAGAGAGGTCTTCGAGATTGAACGACTTAA 420
 DB 361 AAGCTGATCCAGCCATGCGCGGTGTGAGAGAGGTCTTCGAGATTGAACGACTTAA 420
 QY 421 GTTGGGAGGAAGGTTGTAGATTAACTCTGCAATTTTGAAGCTTCCAGAGATTAAGC 480
 DB 421 GTTGGGAGGAAGGTTGTAGATTAACTCTGCAATTTTGAAGCTTCCAGAGATTAAGC 480
 QY 481 ACCGGCTAACTCTGTGCACAGCGCGGTATATACAGAGGCTCAAGCTTATCGGAAT 540
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 QY 541 TACTGGGCTTAACCGCGGTAGGTGTTGTTAAGTTGATGATGAAATCCCGGCGCTCA 600
 DB 541 TACTGGGCTTAACCGCGGTAGGTGTTGTTAAGTTGATGATGAAATCCCGGCGCTCA 600
 QY 601 ACCTGGGAATGCTCAAACTGACTGATAGATGATGATGATGATGATGATGATGATGATGAT 660
 DB 601 ACCTGGGAATGCTCAAACTGACTGATAGATGATGATGATGATGATGATGATGATGATGAT 660

QY 661 TGTGTAGCGGTGAATGCGTATATAGAGAAACACCACTGCGGAAAGCGCACCTG 720
 DB 661 TGTGTAGCGGTGAATGCGTATATAGAGAAACACCACTGCGGAAAGCGCACCTG 720
 QY 721 GACTTAATCTGACACTGAGGTGGGAAAGCGTGGGAGCAACAGGATATGATGATGAT 780
 DB 721 GACTTAATCTGACACTGAGGTGGGAAAGCGTGGGAGCAACAGGATATGATGATGAT 780
 QY 781 AGTCCACGCGGTAAAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
 DB 781 AGTCCACGCGGTAAAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
 QY 841 CTAAAGCTTAATTAATGAGCGCTGGGAGATGAGCGGCAAGGTTAAATCTAAATGAT 900
 DB 841 CTAAAGCTTAATTAATGAGCGCTGGGAGATGAGCGGCAAGGTTAAATCTAAATGAT 900
 QY 901 GACGGGGGCGCGGACAAAGCGGTGAGCATGTGTTAAATTCGAAGCAACGCGAAACCT 960
 DB 901 GACGGGGGCGCGGACAAAGCGGTGAGCATGTGTTAAATTCGAAGCAACGCGAAACCT 960
 QY 961 TACCAAGGCTTGAATCAATCAATGATGATGATGATGATGATGATGATGATGATGAT 1020
 DB 961 TACCAAGGCTTGAATCAATCAATGATGATGATGATGATGATGATGATGATGATGAT 1020
 QY 1021 AGACAGGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1070
 DB 1021 AGACAGGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1070

RESULT 2

AB076131 ID AB076131 standard; DNA, 1424 BP.

AC AB076131:

XX 13-JAN-2003 (first entry)

DE Rhodococcus AM12 16S rRNA DNA.

XX Plasmid stability protein; replication protein; ethylene forming enzyme;

KW carotenoid biosynthesis enzyme; isoprenoid; pyruvate decarboxylase;

KW polyhydroxyalkanoic acid synthase; PHA synthase; nitrile hydratase;

KW alcohol dehydrogenase; terpene synthase; cholesterol oxidase;

XX shuttle vector; 16S rRNA; ds.

OS Rhodococcus erythropolis.

XX W020025709-A2.

XX 18-JUL-2002.

XX 12-DEC-2001; 2001WO-US47868.

XX 12-DEC-2000; 2000US-254868P.

XX (DUPO) DU PONT DE NEMOURS & CO E. I.

XX Bramucci MG, Cheng Q, Kostichka KN, Tomb J;

XX WPI; 2002-557827/59.

XX New nucleic acid molecule encoding replication protein/plasmid

XX stability protein, useful in cloning and expression vectors;

XX particularly shuttle vectors for expression of heterologous genes in

XX Rhodococcus species

XX Example 1; Page 83-84; 96pp; English.

XX This invention describes a novel nucleic acid encoding a replication

XX protein or a plasmid stability protein. The product of the invention is

XX useful for expression of nucleic acid such as genes encoding enzymes

XX involved in the production of isoprenoid molecules, polyhydroxyalkanoic

GenCore version 5.1.6
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OK nucleic - nucleic search, using sw model

Run on: January 30, 2004, 08:32:25 ; Search time 316.06 Seconds
(without alignments)
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Gapop 10.0, Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0 %
Maximum Match 100 %
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1070	100.0	1070	22	AAH25692
2	990	92.5	1424	22	ABQ76131
3	985.2	92.1	1501	22	AA164997
4	985.2	92.1	1501	22	AA164998
5	985.2	92.1	1501	22	AAH77497
6	985.2	92.1	1501	22	AAH2097
7	985.2	92.1	1501	23	AA164177
8	985.2	92.1	1501	24	AA139554

Result No.	Score	Query Match	Length	ID	Description
9	985.2	92.1	1501	24	AA167771
10	985.2	92.1	1501	22	AA166302
11	982.8	91.9	1281	22	AA190025
12	976	91.2	1480	24	AA150855
13	972.8	90.9	1480	24	AA150856
14	918.8	85.9	1518	17	AA118764
15	907.4	84.8	1467	22	AA111023
16	872.4	81.5	1535	20	AA183571
17	856	80.0	1537	19	AA124291
18	830.6	77.6	1485	22	AA125691
19	821.4	76.8	1528	20	AA183570
20	818.2	76.5	1535	20	AA183568
21	815	76.2	1529	20	AA183567
22	815	76.2	1535	20	AA183569
23	813.4	76.0	1529	20	AA183565
24	813.4	76.0	1529	20	AA183566
25	808.6	75.6	1529	20	AA183564
26	808	75.5	15105	20	AA14989
27	807	75.4	1494	25	ABX16312
28	806.6	75.4	1489	24	ABX1632
29	801	74.9	1487	22	AA11034
30	798.4	74.6	1542	17	AA129140
31	798.4	74.6	1542	22	AA175410
32	798.4	74.6	1542	22	AA162270
33	798.4	74.6	1542	24	ABN85800
34	798.4	74.6	15097	20	AA124983
35	798.4	74.6	15098	20	AA124984
36	798.2	74.6	1540	20	AA191514
37	797.8	74.6	1506	24	ABX71613
38	797.2	74.5	1541	20	AA124986
39	796.8	74.5	1542	20	AA123015
40	795.2	74.3	1461	24	ABX1620
41	793.6	74.2	15014	20	AA124987
42	793.4	74.1	1473	17	AA118760
43	792	74.0	1528	22	AA176235
44	792	74.0	1542	14	AA164119
45	792	74.0	1566	17	AA118645

ALIGNMENTS

RESULT 1
AAH25692
ID AAH25692 standard; DNA; 1070 BP.
AC AAH25692;
XX
DT 05-SEP-2001 (first entry)
XX
DE Nucleotide sequence of 16S rRNA of *Pseudomonas* sp.
XX
KW 16S rRNA; anti-freeze protein; food additive; frozen vegetable;
frozen confectionery; ss.
XX
OS *Pseudomonas* sp.
XX
XX
XX WO200144275-A2.
XX
XX 21-JUN-2001.
XX
XX 05-DEC-2000; 2000WO-EP12396.
XX
XX 05-DEC-1999; 99GB-0029696.
XX
XX 15-DEC-1999; 99GB-0029696.
XX
XX (UNIT) UNILEVER PLC.
XX (UNIT) UNILEVER NV.
XX (HIND-) HINDUSTAN LEVER LTD.
XX
XX Berry M., Griffiths A., Hill P., Laybourne-Parry J., Mills S.;
XX WPI; 2001-398120/42.
XX


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Db      601 GGGAACTGCATTGAAAACCTGACTAGAGTATGTTAGAGGGTGTGGAATTTCCTGTG 660
QY      665 TAGCGTGAAATGCGTAGATATAGAGAGAACCAAGTGGCGAAGCCACCACTGTGACT 724
Db      661 TAGCGGTGAATGCGTAGATATAGAGAGAAATACCAAGTGGCGAAGCCACCACTGTGACT 720
QY      725 AATAGTGACACTGAGGTGGGAAAGCGTGGGAGCAAAACGATTAATACCTGTGTAGTC 784
Db      721 AATAGTGACACTGAGGTGGGAAAGCGTGGGAGCAAAACGATTAATACCTGTGTAGTC 780
QY      785 CAGCGCGTAAACGATGTCACTAGCCGTTGGAAGCCTTGAGCTTTAGTGGCGAGCTAA 844
Db      781 CAGCGCGTAAACGATGTCACTAGCCGTTGGAAGCCTTGAGCTTTAGTGGCGAGCTAA 840
QY      845 CGCATTAAGTTGACCGCTGGGAGTACGGCCGCAAGTTAAACTCAATGAATTGACG 904
Db      841 CGCATTAAGTTGACCGCTGGGAGTACGGCCGCAAGTTAAACTCAATGAATTGACG 900
QY      905 GGGGCCCGCACAGCGGTGAGCATGTGTTAATTGAGCAACGCGAAGAACCTTACC 964
Db      901 GGGGCCCGCACAGCGGTGAGCATGTGTTAATTGAGCAACGCGAAGAACCTTACC 960
QY      965 AGGCTTTGACATCCAAATGAATCTTTAGAGATGATTGTGCTTCGGAACATTGAGAC 1024
Db      961 AGGCTTTGACATCCAAATGAATCTTTAGAGATGATTGTGCTTCGGAACATTGAGAC 1020
QY      1025 AGGTGCTGCATGCTGCTGCTGAGCTGCTGCTGTTGGAATGTAGG 1068
Db      1021 AGGTGCTGCATGCTGCTGCTGAGCTGCTGCTGAGATGTGGG 1064

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Search completed: January 30, 2004, 22:02:57
 Job time : 4088.5 secs

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 ACCESSION AF451270.1 GI:18092524
 VERSION
 KEYWORDS
 SOURCE Pseudomonas sp. E102
 ORGANISM Pseudomonas sp. E102
 Pseudomonadaceae; Pseudomonas.
 REFERENCE 1 (bases 1 to 1483)

AUTHORS Spanggaard, B., Huber, I., Nielsen, U., Sick, E. B., Pipper, C. B.,
 TITLE Martinussen, T., Slienderrecht, W. J., and Gram, L.
 JOURNAL The probiotic potential against vibriosis of the indigenous
 MEDLINE Microflora of rainbow trout
 PUBMED Environ. Microbiol. 3 (12), 755-765 (2001)
 21835725
 11846765
 2 (bases 1 to 1483)
 REFERENCES Spanggaard, B., Huber, I., Nielsen, U., Sick, E. B., Pipper, C. B.,
 Martinussen, T., Slienderrecht, W. J., and Gram, L.
 TITLE Direct Submission
 JOURNAL Submitted (22-NOV-2001) Department of Seafood Research, c/o
 Technical University of Denmark, Danish Institute for Fisheries
 Research, Soltofte Plads, Kongens Lyngby, Copenhagen DK-2800,
 Denmark
 FEATURES
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 Best local Similarity 99.2%; Pred. No. 0;
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REFERENCE 2 (bases 1 to 1470)
AUTHORS Godfrey,S.A.C., Harrow,S.A., Marshall,J.W. and Klena,J.D.
TITLE Direct Submission
SUBMITTED (28-NOV-2000) Integrated Crop Protection, Crop & Food
RESEARCH Ltd., Private Bag 4704, Christchurch 8152, New Zealand
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BASE COUNT 373 a 325 c 456 g 314 t 2 others
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Query Match 98.5%; Score 1054.4; DB 1; Length 1470;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 1058; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

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QY 903 CGGAGGCGCGGACAGAGCGGTGAGATGATGATGATGATGATGATGATGATGATGATGAT 962
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ACCESSION AF057645
VERSION AF057645.1 GI:3047379
KEYWORDS Pseudomonas libanensis
SOURCE Pseudomonas libanensis
ORGANISM Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
REFERENCE 1 (bases 1 to 1516)
AUTHORS Daboussi,F., Hamze,M., Elomari,M., Verhille,S., Baïda,N., Izard,D.
and Leclerc,H.
TITLE Pseudomonas libanensis sp. nov., a new species isolated from
Lebanese spring waters
JOURNAL Int. J. Syst. Bacteriol. 49 Pt 3, 1091-1101 (1999)
MEDLINE 99354498
PUBMED 10425766
REFERENCE 2 (bases 1 to 1516)
AUTHORS Daboussi,F., Hamze,M., Verhille,S., Baïda,N., Izard,D. and
Leclerc,H.
TITLE Direct Submission
JOURNAL Submitted (07-Apr-1998) Bacteriological Laboratory, Medical
University, 1 place de Verdun, Lille 59045, France
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Best Local Similarity 99.2%; Pred. No. 0;
Matches 1057; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 3 CCTTGCCTCAGATTGAACGCTGCGCGAGGCTTAACATGCAAGTCGAGCGGTAGAGAGA 62
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 ACCESSION AF267911
 VERSION AF267911.1 GI:9623379
 KEYWORDS
 SOURCE Pseudomonas synxantha
 ORGANISM Pseudomonas synxantha
 Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 Pseudomonadaceae; Pseudomonas.
 1 (bases 1 to 1500)
 Pirttila,A.M., Laukkanen,H., Pospiech,H., Myllyla,R. and Hohnola,A.
 Detection of intracellular bacteria in the buds of Scotch pine
 (Pinus sylvestris L.) by in situ hybridization
 Appl. Environ. Microbiol. 66 (7), 3073-3077 (2000)
 JOURNAL MEDLINE 20356462
 PUBMED 10877808
 REFERENCE 2 (bases 1 to 1500)
 AUTHORS Pirttila,A.M., Laukkanen,H., Pospiech,H., Myllyla,R. and Hohnola,A.

TITLE Direct Submission
 JOURNAL Submitted (15-MAY-2000) Department of Biology/Botany, University of
 Culu, POB 3000, Culu FIN-90014, Finland
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 Matches 1060; Conservative 0;

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the Fluorescent Pseudomonads
 Unpublished
 Reference 2 (bases 1 to 1355)
 Authors Gaidick, M., Plasmeyer, M.L., Blaine, L.D., Pienta, P.A. and
 Gillevet, P.M.
 Title Direct Submission
 Submitted (25-SEP-1998) Microbial Authentication Resource, American
 Type Culture Collection, 10801 University Blvd, Manassas, VA
 20110-2209, USA

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 LOCUS AX175617 1140 bp DNA linear PAT 03-JUL-2001
 DEFINITION Sequence 5 from Patent WO0144275.
 ACCESSION AX175617
 VERSION AX175617.1 GI:14598936
 KEYWORDS
 SOURCE
 ORGANISM
 Pseudomonas synxantha
 Pseudomonas synxantha
 Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 Pseudomonadaceae; Pseudomonas.
 REFERENCE
 1 Berry, M.J., Griffiths, A.U., Hill, P.J., Laybourne-Parry, J. and
 Mills, S.V.
 Processes and organisms for the production of anti-freeze proteins
 Patent: WO 0144275-A 5 21-JUN-2001;
 TITLE
 JOURNAL
 FEATURES
 source
 1..1140
 /organism="Pseudomonas synxantha"
 /mol_type="genomic DNA"
 /db_xref="taxon:47883"

BASE COUNT 296 a 239 c 354 g 251 t
 ORIGIN

Query Match 98.7%; Score 1056.4; DB 6; Length 1140;
 Best Local Similarity 99.4%; Pred. No. 0;
 Matches 1060; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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 Db 11 CTTGCTCAGATTGAACGCTGCGGAGGCTTAACACATGCAAGTGAAGCGGTAGAGAGA 70
 QY 63 AGCTTGCTTCTTGAAGAGCGGCGAGGCTGATTAATGCTTGAATCTGCTGTAGT 122
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 QY 123 GGGGATTAACGTTGCGAAGACGAGCTTAATACGCTTACGCGGAGAAAGAGAGG 182
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 QY 243 TGGCTCAACAAAGGCGAGATCCGTAATGCTGAGAGGATGATCAGTCACTGGAAGT 302
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Qy 843 AACGCATTAGTTGACCGCTGGGGAGTACGGCCGCAAGTTAAACTTAATTAATTGA 902
Db 851 AACGCATTAGTTGACCGCTGGGGAGTACGGCCGCAAGTTAAACTTAATTAATTGA 910
Qy 903 CGGGGGCCCGCAACAAGCGGTGAGCAATGTGTTAATTCGAAGCAACGGCAAGACTTA 962
Db 911 CGGGGGCCCGCAACAAGCGGTGAGCAATGTGTTAATTCGAAGCAACGGCAAGACTTA 970
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RESULT 8
LOCUS AY014824 1461 bp DNA linear BCT 30-NOV-2001
DEFINITION Pseudomonas sp. NZ108 16S ribosomal RNA gene, partial sequence.
ACCESSION AY014824
VERSION AY014824.1 GI:17220742
KEYWORDS
SOURCE
ORGANISM Pseudomonas sp. NZ108
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.

REFERENCE
1 (bases 1 to 1461)
Godfrey, S.A.C., Harrow, S.A., Marshall, J.W. and Klena, J.D.
Characterization of *Pseudomonas* species (sensu stricto) causing
'ginger blorch' disease of cultivated *Agaricus bisporus* using 16S
rRNA gene typing
JOURNAL
REFERENCE
2 (bases 1 to 1461)
Godfrey, S.A.C., Harrow, S.A., Marshall, J.W. and Klena, J.D.
Direct Submission
TITLE
JOURNAL
Submitted (28-NOV-2000) Integrated Crop Protection, Crop & Food
Research Ltd., Private Bag 4704, Christchurch 8152, New Zealand
FEATURES
Location/Qualifiers
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/mol_type="genomic DNA"
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/db_xref="taxon:148765"
RNA
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BASE COUNT 372 a 323 c 453 g 311 t 2 others
ORIGIN

Query Match 98.8%; Score 1057.2; DB 1; Length 1461;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 1059; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 3 CCTGTCTCAGATTGAAGCGTGGCGGAGGCTTAACATGCAAGTGAAGCGGTAGAGAG 62
Db 11 CTTGGCTCAAGATTGAAGCGTGGCGGAGGCTTAACATGCAAGTGAAGCGGTAGAGAG 70
Qy 63 AGCTTGCTTCTCTTGAAGCGGCGGAGCGGTGAGTATGCTAGGAATCTGCTGTAGT 122
Db 71 AGCTTGCTTCTCTTGAAGCGGCGGAGCGGTGAGTATGCTAGGAATCTGCTGTAGT 130
Qy 123 GGGGGATAAGCTTGGGAAAGGACGCTAATACCGCATAGTCTCTANGGAGAAACAGAG 182
Db 131 GGGGGATAAGCTTGGGAAAGGACGCTAATACCGCATAGTCTCTANGGAGAAACAGAG 190
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Qy 303 GAGACACGCTCCAGACTCTTACGGAGCGACAGTGGGAAATATTGGCAATGGCGAAA 362
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Qy 423 TGGAGAAAGGCTTGAATTAACTGTGCAATTTGACGTACCGACAGAAATAGCAC 482
Db 431 TGGAGAAAGGCTTGAATTAACTGTGCAATTTGACGTACCGACAGAAATAGCAC 490
Qy 483 CGGCTAACTCTGTGCCAGACCGCGGTAAATACAGAGGTCACAGCTTATCGGAATTA 542
Db 491 CGGCTAACTCTGTGCCAGACCGCGGTAAATACAGAGGTCACAGCTTATCGGAATTA 550
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Qy 963 CCAGGCTTGAATCATCAATGAATCTTTGAGATGATGTTGGCTTCGGGAACATTAG 1022
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Qy 1023 ACAGGTGCTGATGCTGCTGCTGAGCTCGTGTGTAATGTAAG 1068
Db 1031 ACAGGTGCTGATGCTGCTGCTGAGCTCGTGTGTAATGTAAG 1076

RESULT 9
LOCUS AF094729 1355 bp DNA linear BCT 04-OCT-2000
DEFINITION Pseudomonas fluorescens strain ATCC 17566 16S ribosomal RNA gene,
partial sequence.
ACCESSION AF094729
VERSION AF094729.1 GI:10567500
KEYWORDS
SOURCE Pseudomonas fluorescens
Pseudomonas fluorescens
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
REFERENCE
1 (bases 1 to 1355)
Galdick, M., Plasmeyer, M.L., Blaine, L.D., Plenta, P.A. and
Gilliver, P.M.
TITLE Comparison of Phenetic and Phylogenetic Classification Systems for